

60.38; Score 516.4; DB 9; Length 518;

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/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clonetype="S0183b01F"
/clonelib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

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Best Local Similarity 99.8%; Pred. No. 3e-77;
Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Oy 28 taaataaacactcatctatcatgtagatataataataatcgcacacactataaag 87
    |||||||
Db 1 TAAATATTAACACTTTCATTCATGATGATTAATATATATATGACATCATATATAAG 60

Oy 88 taaaacactcatttcccccctcacttatttaaacactatataatgaactac 147
    |||||||
Db 61 TAAACACTCTCATTTCTCCCTCCCTCATTTTATTACACACTTATATATGAACTAC 120

Oy 148 tataagcctacaccggttgcgtactgatatcataaatggttataatlaacta 207
    |||||||
Db 121 TATAGGCATCATCCCGTTCGTTACTCGATCATAAAGTGTATTAAATTAATTA 180

Oy 208 tagatgcataaattccatcaagatagatataatggttataaagaagaacacatc 267
    |||||||
Db 181 TAGATGCATTAATTCATCATCAGAGTATGCATATCATTTGTTATTAAGAAACACATC 240

Oy 268 taaagttcttctcctcgcaagcactctccctctgacaattgtagaaaactgcgccacg 327
    |||||||
Db 241 TAAACTCTTCTTCCCTCCCGACGACCTCCCTGTGACAAATTTAGAAAACTCGGCGCACG 300

Oy 328 ggaagcgccgaagttagatctcagaacactcggaagtgtgaattctgcgccacct 387
    |||||||
Db 301 GGAAGCGCGAGATGTAGATCTCAGCAAACTCGCAGTGTGAAGTTCTGGCGCACCT 360

Oy 368 ggtgcatacactgtttgctgcgaagctgtcgaaaacataataaacagacagatgaatt 447
    |||||||
Db 361 GGTGCATACACTGTTGCTGCGCAAGCTGTGAAACAAATATTAACACGACAGATGAAT 420

Oy 448 cctgcagtggaacttggaatttcgtaacacacatctcatgccaagaagtgttcacgt 507
    |||||||
Db 421 CCTGAGTGGGCACTTGATTTTCGTAAACACACAAATCTCATTTGCCAAAGTTGTCCAGTT 480

Oy 508 gtagcagagatcatcagtcacacacacatggaatatc 545
    |||||||
Db 481 GCAGCAGGATATCATGTCACCAACCAATGAGATATTC 518

RESULT 2
AV562377 494 bp mRNA linear EST 07-SEP-2000
LOCUS AV562377 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone S0169D07F 3', mRNA sequence.
ACCESSION AV562377
VERSION AV562377.1 GI:8733803
KEYWORDS EST.
SOURCE Arabidopsis thaliana
ORGANISM thale cress.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 494)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
SOURCE Location/Qualifiers
1. 494
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="S0169D07F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 155 a 113 c 81 g 145 t
ORIGIN

Query Match 57.7%; Score 494; DB 9; Length 494;

Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 29 aaataaacactcatctatcatgtagatataataataatcgcacacactataaagt 88
    |||||||
Db 1 AAATATTAACACTTTCATTCATGATGATTAATATATATGACATCATATATAAGT 60

Oy 89 aaaaacactcatttcccccctcacttatttaaacactatataatgaactact 148
    |||||||
Db 61 AAACACTCTCATTTTCTCCCTCCCTCATTTTATTACACTTATTAATGAACACTACT 120

Oy 149 ataggcatcaccggttgcgtactcgtatcataaaatggttattaaatlaactatc 208
    |||||||
Db 121 ATAGGCATCATCCCGTTCGTTACTCGATCATAAAGTGTATTAAATTAATTA 180

Oy 209 agatgcataaatctcatcaagaagtatgcaatatcaattggtataaagaagaagccactc 268
    |||||||
Db 181 AGATGCATTAATTCATCATCAGAGTATGCATATCATATGTTATTAAGAAAGACATCT 240

Oy 269 aaagttcttctcctcgcaagcactctccctctgacaattgtagaaaactgcgccacg 328
    |||||||
Db 241 AAAGTCTTCTTCTCCCGACGACCTCCCTGTGACAAATTTGAGAAACTGGGCGCACG 300

Oy 329 gaaagcggaagttagatctcagaacactcggaagtgtgaattctgcgccacctg 388
    |||||||
Db 301 GAAAGCGGAGATTTGATCTCAGCAAACTCGCAGTGTGAAGTTCTGGCGCACCTG 360

Oy 389 gtgcatacactgtttgctgcgaagctgtcgaaaacataataaacagacagatgaattc 448
    |||||||
Db 361 GTGCATACACTGTTGCTGCGCAACCTGTGCAAAATATTAACGACGACAGATTAATTC 420

Oy 449 ctgcagtggaacttggaatttcgtaacacacatctcatgccaagaagtgttcacgtg 508
    |||||||
Db 421 CTGCAGTGGGCACTTGATTTTCGTAAACACACAAATCTCATTTGCCAAAGTTGTCCAGTTG 480

Oy 509 tagcagagatcatc 522
    |||||||
Db 481 TAGCAGGATATCA 494

RESULT 3
BE590867/c 551 bp mRNA linear EST 18-AUG-2000
LOCUS BE590867 WHE0855_C01_E01S wheat 20-45 DAP spike cDNA library Trilicium
DEFINITION aestivum cDNA clone WHE0855_C01_E01, mRNA sequence.
ACCESSION BE590867
VERSION BE590867.1 GI:9845940
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 551)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes - 20-45 DAP spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
```


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Tel: 5105595773
Fax: 5105595818

Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stragene SK primer.

FEATURES

source 1..505
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0963_B10.C19"
/clone.lib="Wheat pre-anthesis spike cDNA library"
/tissue.type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli S01R"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site.1: EcoRI; Site.2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pluscript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 99 a 148 c 160 g 98 t

ORIGIN

Query Match 23.2%; Score 198.4; DB 10; Length 505;
Best Local Similarity 67.3%; Pred. No. 5.3e-24;
Matches 280; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 364 ggtgtgaattcttgcggccaccctggtgcatacactgttgcctgccaagctgtgaaac 423
DB 504 ggtgtgaattcttgcggccaccctggtgcatacactgttgcctgccaagctgtgaaac 445
QY 424 aatataacacgacacgaatcctcgtcagtgaggactggatttctgtaacacacac 483
DB 444 agtagcagacacgacacgaatcctcgtcagtgaggactggatttctgtaacacacac 385
QY 484 tcaatgcacaaagtgtgtcagttgtagcaggatatacagtaacacacacacacacac 543
DB 384 tccctgcccgaacgacgacacgacgacgacgacgacgacgacgacgacgacgacgac 325
QY 544 tctcggaaggtgaggtgtcctgtagacttggaacatcgtgacacacacacacacac 603
DB 324 tccctgaaggtgaggtgtcctgtagacttggaacatcgtgacacacacacacacac 265
QY 604 aagttcctcaggtctcttcacacacacacacacacacacacacacacacacacacac 663
DB 264 aaggtcctcaggtctcttcacacacacacacacacacacacacacacacacacacac 205
QY 664 cttagatccaagacatagtcacactctcttgcgcaataagtaacacacacacacacac 723
DB 204 ttgagcttcgacacgcttgtagacacgcttgtagacacgcttgtagacacgcttgtag 145
QY 724 cttatataaaggaatgaagaagcttcacacacacacacacacacacacacacacacac 779
DB 144 cggagcgaaggggtcgcagcagcttcacacacacacacacacacacacacacacacac 89

RESULT 6
BF483056/c 491 bp mRNA linear EST 06-DEC-2000
LOCUS WHE2314_C03_E06ZS wheat pre-anthesis spike cDNA library Triticum
DEFINITION WHE2314_C03_E06ZS wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE2314_C03_E06, mRNA sequence.
ACCESSION BF483056
VERSION BF483056.1 GI:11566357

KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 491)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

, P.S., Hsia, C.C., Kang, Y., Iazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat

genomes - Pre-anthesis spike cDNA library

Unpublished (2000)

JOURNAL Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stragene SK primer.

FEATURES

source 1..491
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2314_C03.E06"
/clone.lib="Wheat pre-anthesis spike cDNA library"
/tissue.type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli S01R"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site.1: EcoRI; Site.2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pluscript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 93 a 145 c 151 g 101 t

ORIGIN

Query Match 23.0%; Score 196.8; DB 10; Length 491;
Best Local Similarity 67.5%; Pred. No. 9.9e-24;
Matches 276; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 371 agttctgycgacacccctgtgatacactgttgcctgccaagctgtgaaacacacacacacac 430
DB 491 agttctgycgacacccctgtgatacactgttgcctgccaagctgtgaaacacacacacac 432
QY 431 acacgaacagatgaatcctcgtcagtgaggacttgatcttgcgaacacacacacacacac 490
DB 431 gcaacgaacagatgaatcctcgtcagtgaggacttgatcttgcgaacacacacacacac 372
QY 491 caaaggtgttcagttgtagcaggatatacagtaacacacacacacacacacacacacac 550
DB 371 ncaagatcaccacagttgtgacgggagatgctgacacacacacacacacacacacacac 312
QY 551 ggtgaggtgttgcagtgacttggaacacacacacacacacacacacacacacacacacac 610
DB 311 ggtgaggtgttgcagtgacttggaacacacacacacacacacacacacacacacacacac 252
QY 611 tgaaggtcttcac 670
DB 251 tcatctcatgttcgacgac 192
QY 671 ccaagcattagtaac 730

Db 605 TATAGTGCTATGGCTATGTAGCTAGCGTCTTCTTGACGCGGTTCTCTGTGACATGCA 546
 Qy 311 agaaacacacgagcagcaggaagccgagatcttagatcccaacacacgagcttga 370
 Db 545 AGTAAACACACGACACGAGGAGACCAAGATCATCTGTGACGAAATTCGAGTGTGA 486
 Qy 371 agcttcgagcagccctgg---tgacatacctgttgcctgcgaacgctgcgaacaata 427
 Db 485 AGTAATCCCTGTAAGATGTGATGCTGTCACTGATCTCTATCTCTTGTTCGATAGAA 426
 Qy 428 taacacgacagatgaatctctgcagctgagcttgatcttcgttaacacacatctcat 487
 Db 425 CAACACCAACCTGTGTATATATATATTTGGCTTTGTATCTCATAGCTACTCTTCT 366
 Qy 488 tcccaagatcttccagcttgtagcagagatcatcagcccaacacatgagatcttc 547
 Db 365 TCCCAATGTAGCATCTGTGTTCGAGATATCTGTCAACATCCAGTGCAGATGTTTC 306
 Qy 548 ggaagtgagggcttgtagacttgagacatctgataccacataacaaagatagaaat 607
 Db 305 TTAGATTAAGATACACTAGGCGCAGCAAGATCAAGGCTGTGTATCACAGTGTAGAGG 246
 Qy 608 tctcagagctctccacacatcacaactcgaactctgctgttgaactgagaaagcctta 667
 Db 245 ACCTCATGTCCACCATCATATCTCAACTTTGGCTTGTGATAGTGAAGGAGGAAAA 186
 Qy 668 gatccacgacattagtcacactcctcttgagcacaagtaacattagatgactcat 727
 Db 185 ACTCATGCGCATTTGAAGACTTGTCTTGTGTGTAACCTCAGACGATTTTCATCTTGTG 126
 Qy 728 taaacgataaagaacgacttccacaacactcgttactataaagaggctcttataatta 787
 Db 125 TTAAGGAATCAAGAACTCTCTATCATCTTCCACAAATGAGTGTCTTGTGACATTC 66
 Qy 788 tagacatct 796
 Db 65 TTGCCATTTT 57

RESULT 9
 BM407295/c 718 bp mRNA linear EST 22-JAN-2002
 LOCUS EST81622 potato roots Solanum tuberosum cDNA clone cPRO30M16 5'
 DEFINITION end, mRNA sequence.
 ACCESSION BM407295
 VERSION BM407295.1 GI:18258925
 KEYWORDS EST
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 718)
 van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
 Uterback,T., Chelmingo,A., Bougri,O., Buell,C.R., Romling,C.,
 Tanksley,S. and Baker,B.
 Generation of ESTs from potato roots
 Unpublished (2001)
 TITLE Contact: Research Genetics, Libraries Division
 JOURNAL Tel: 1-800-711-6195
 COMMENT Email: cdna@resgen.com
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: 73.

FEATURES
 Source
 1..718
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cPRO30M16"
 /clone_lib="potato roots"
 /tissue_type="roots"
 /dev_stage="in vitro grown stem cuttings"

/lab_host="SOLR"
 /note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; supplier: Cornell University, Tanksley lab;
 sequencing: The Institute for Genomic Research. Roots were
 isolated from in vitro grown stem cuttings on CM medium.
 Roots were isolated two weeks after placing the stem
 cuttings from in vitro grown plants on medium."
 BASE COUNT 243 a 128 c 142 g 205 t
 ORIGIN

Query Match 20.2%; Score 173.2; DB 10; Length 718;
 Best Local Similarity 60.2%; Pred. No. 7.7e-20;
 Matches 324; Conservative 0; Mismatches 208; Indels 6; Gaps 2;

Qy 273 tctcttcctccgagcagcactcctcctcgcacatctgagaactcgcgcaggaag 332
 Db 565 TCATCTTCTTTCAGCAGCATTTCTCTTGGCATTTAAAGTACAGCAGCAACAGGGA 506
 Qy 333 gccgagatctgagatctcagcaactcgcgagctgtagaagcttcgcgcacccctgtgc 392
 Db 505 ACCCAATTCATTTTCTGTCGCAATTTTGGAGTTGAATGATCTCTTGTACTGTGA 446
 Qy 393 ataacctgttgcctgc---aagctgtcgaacaataataaacagacagatgattcc 449
 Db 445 TTTCACTGTTTGTCTTCTCTATTTTCCATATTAATAGCAACACCTATGATGATCC 386
 Qy 450 tgcagtgagacttgagatcttgcgaacacacatcattcgaaggttgctcagttgt 509
 Db 385 GATCACTGTTTGTGACATCTGATGCTCACTATCTTTTCCAAAAGACATCACTTGA 326
 Qy 510 agcaggatatacagtcac 569
 Db 325 ACCAGGAATATCTGTCAACATTCAGTGAGGAGTGTCCCTTAAGTAAAGATCACTAGAC 266
 Qy 570 tggacatcttgatccacacataacacacacacacacacacacacacacacacacac 629
 Db 265 TGGACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 206
 Qy 630 ctcaactcttgagcttcttgagacacacacacacacacacacacacacacacacac 689
 Db 205 CTCACACAGAGCTTAGAAGCAATGATGAGGAGGATGCTCTGACCATTTAAACCTTG 146
 Qy 690 t---cttgccataaglaacactttagagtgatgtatctataaagacacacacacac 746
 Db 145 TTGCTTCAAT 86
 Qy 747 tccaacactcgtcttaacataaagaggtctcttataattatagaacatcttgatctt 804
 Db 85 TCCAAATCACTTTGCAACAATAAGTGTTCATATCTTCAACAGACATATGATCCTT 28

RESULT 10
 BH558079/c 395 bp DNA linear GSS 14-DEC-2001
 LOCUS BOGFM69TF BOGF Brassica oleracea genomic clone BOGFM69, DNA
 DEFINITION sequence.
 ACCESSION BH558079
 VERSION BH558079.1 GI:17809859
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 395)
 Town,C.D., Van Aken,S., Uterback,T. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 JOURNAL other GSSs: BOGFM69TR
 COMMENT Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtonnet@tr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..395

/organism="Brassica oleracea"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOGFM69"
 /clone_1ib="BOGF"
 /note="Vector: PHOS1; Site.1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
 BASE COUNT 107 a 81 c 85 g 122 t
 ORIGIN

Query Match 17.6%; Score 150.8; DB 12; Length 395;
 Best local Similarity 80.7%; Pred. No. 5.4e-16;
 Matches 176; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 274 ctctctctcgcagcagcactctcctctgacaattgtagaanaactgagccaggaag 333
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 DB 386 CTCTCTCTCCGCGAGCATCTCTCACTGACAGTTGAAGTAACAGCAGCGGAGGA 327
 QY 334 ccgaagtttgaagtttcagaaactcgaggtgttgaagttctggccacccctgtgca 393
 |||||
 DB 326 CCAGAGTTTGAATCTCAGAGAACTCAGAGTTGTGAACCTTTGCCACTGAGTGCA 267
 QY 394 taacagtttgcctcgaacactgtcgaataaacaacagacagatgaattcctgca 453
 |||||
 DB 266 TAACAGTTTGTCTTCGAGATTTCGGAACATATCATCATCGACTCGGTGATTTGAA 207
 QY 454 gtggagacttgatttcgttaacacaaatcctcaatgcc 491
 |||||
 DB 206 GTGGAGATGATGATTCTGTAGTACACCACTCATTTGCC 169

RESULT 11
 BE602964/c 520 bp mRNA linear EST 22-OCT-2001
 LOCUS
 DEFINITION
 HVSMEH0101D16f Hordeum vulgare 5-45 DAP spike EST library
 HVCNNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0101D16f,
 mRNA sequence.

ACCESSION BE602964
 VERSION BE602964.3 GI:16322734
 KEYWORDS EST.
 SOURCE
 ORGANISM

Hordeum vulgare
 barley.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 520)
 Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton
 , R. D., Close, S. J., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 5-45 DAP spike cDNA library
 Unpublished (2001)
 On Aug 21, 2000 this sequence version replaced gi:13190740.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 405
 Seq primer: AATTACCTTCACCTAAAGG
 High quality sequence stop: 513.
 Location/Qualifiers

source

1..520
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEH0101D16f"
 /clone_1ib="Hordeum vulgare 5-45 DAP spike EST library
 HVCNNA0009 (5 to 45 DAP)"
 /tissue_type="5-45 DAP spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
 Plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close). Whole
 spikes with awns trimmed were collected at 5, 10, 15, 20,
 30 and 45 DAP (Fenton). Total RNA was prepared from each
 pool, equal quantities of all six RNA pools were combined,
 poly(A) RNA was purified from the mixture, one primary
 unamplified cDNA library was made, and 1 million plv were
 in vivo excised to give phagescript SK(-) cDNA phagemids
 (Choi) in the TJ Close lab at the University of California,
 Riverside. Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)"
 BASE COUNT 84 a 108 c 184 g 84 t
 ORIGIN

Query Match 17.1%; Score 146.8; DB 10; Length 520;
 Best local Similarity 60.6%; Pred. No. 2.3e-15;
 Matches 241; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 381 ccaacctggtgcatacactgttgcctgcgaagctgcgaacaataaacaacgacag 440
 |||||
 DB 520 CCACCCCGGGGCGTACACCGTGTGCGCGAGTGTGGAAGACGAAACACACTCG 461
 QY 441 atgaattcctgcagtggaattgttgcgaacacaaatcattgcgaagttgt 500
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 DB 460 GTGGATCCCGAGCACCGCGCGCGCCCTCTGTACACACAACCTCGGTACCAAGACAC 401
 QY 501 tccagttgtagcagagatcagatcagtcacacaaatgaagatattctcgaggtgaggtt 560
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 DB 400 TCTGTGTGTCGCGGAGTGTGCGTACACCACTGCAAGTACTCTTAAGGCTGGGTC 341
 QY 561 gctagagacttgaacacttgatccacacataaagaatagaagttcttgagttctc 620
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 DB 340 GCTGGGGCTTGGAGCATCCGGATCCACATCAGGAGGTGAAGAGTGGCATGTCCG 281
 QY 621 tccacaaatcgaacttgcgtgttgaacctggaagagcccttagatccaagcatt 680
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 DB 280 GCCGCGACCTCGACGCGCGGTGTGCGGAGTGGCGGAGCGCGGAGCTCGCAGCGCTT 221
 QY 681 agtcaactctcttggcacaatgaacttaagatgattgattatataagagatgaag 740
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 DB 220 GGCCAGTCTCTGGAGCGGTGACCGGACCGGAGGCGGCGGACGAGAGGGTCCAC 161
 QY 741 aacgtctcaacaacactctgcttactataaagaaggtctc 778
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 DB 160 CAGTGGCGATCACCGCGCCCAACACACAGCGGTGCC 123

FEATURES
 Location/Qualifiers

RESULT 12
 BF259482/c

LOCUS 574 bp mRNA linear EST 22-OCT-2001
DEFINITION HSMET0019D18f Hordeum vulgare seedling root EST library HVCNDA0007
(Etiolated and unstressed) Hordeum vulgare cDNA clone
ACCESSION HSMET0019D18f, mRNA sequence.
VERSION BF259482
KEYWORDS
SOURCE
ORGANISM
barley.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
; Trilicaceae; Hordeum.
REFERENCE 1 (bases 1 to 574)
AUTHORS Wang, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
JOURNAL On Nov 16, 2000 this sequence version replaced gi:1118511.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 426
Seq primer: AATTAACCTCCTACCTAAGG
High quality sequence start: 572.
Location/Qualifiers
1..574
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HSMET0019D18f"
/clone_1id="Hordeum vulgare seedling root EST library
HVCNDA0007 (Etiolated and unstressed)"
/isuse_type="Seedling root"
/lab_host="TJc121"
/note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedling roots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give pBluescript
SK(-) cDNA phagemids. These steps were performed in the TUG
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wang). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wang, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders
Also see Close TJ, Wang R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30
(http://wheat.pw.usda.gov/99pages/bgn/31/cover.html)"
BASE COUNT 150 a 141 c 131 g 152 t
ORIGIN

Query Match	16.7%;	Score 143;	DB 10;	Length 574;
Best Local Similarity	-60.4%;	Pred. No. 9.5e-15;		
Matches 236;	Conservative	0;	Mismatches 155;	Indels 0;
			Gaps	0;

[illegible]

FEATURES	Source
DEFINITION	BH542868 773 bp DNA linear GSS 14-DEC-2001
LOCUS	BH542868/c
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	Brassica oleracea.
ACCESSION	BH542868
VERSION	BH542868.1
KEYWORDS	GI:17794649
SOURCE	GSS.
ORGANISM	Brassica oleracea.
ORGANISM	Brassica oleracea.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ORGANISM	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ORGANISM	Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
ORGANISM	1 (bases 1 to 773)
ORGANISM	Town,C.D., Van Aken,S., Uteirpaek,T. and Fraser,C.M.
ORGANISM	Whole genome shotgun sequencing of Brassica oleracea
ORGANISM	unpublished (2001)
ORGANISM	Other_GSSs: BCGJN29TR
ORGANISM	Contact: Chris Town
ORGANISM	TIGR
ORGANISM	9712 Medical Center Drive, Rockville, MD 20850, USA.
ORGANISM	Tel: 301-838-3523
ORGANISM	Fax: 301-838-0208
ORGANISM	Email: cdtown@tigr.org
ORGANISM	DNA is from a doubled haploid provided by Tom Osborn.
ORGANISM	Seq primer: TF
ORGANISM	Class: sheared ends.
ORGANISM	Location/Qualifiers
ORGANISM	1..773
ORGANISM	/organism="Brassica oleracea"
ORGANISM	/strain="TO1000DH3"
ORGANISM	/db_xref="taxon:3712"
ORGANISM	/clone="BCGJN29"
ORGANISM	/clone.lib="BCGJ"
ORGANISM	/note="Vector: pHOSt. Site 1: BstXI: 2-3 kb sheared
ORGANISM	genomic DNA inserted into pHOSt using BstXI linkers"
BASE COUNT	214 a 158 c 166 g 235 t
ORIGIN	

Query Match	16.6%;	Score 142.2;	DB 12;	Length 773;
Best Local Similarity	76.7%;	Pred. No. 1.2e-14;		
Matches 174;	Conservative	0;	Mismatches 53;	Indels 0;
				Gaps 0;

Y	265	alttaaatctctctcccccgcagccactctccctctacaattgtaaaaaactgcgccc	324
Db	367	ATCTATGTTCTTCTTCCTCCCGAGCATTTGTCCTCTACAGTTGAATAAAGGACGCC <td>308</td>	308
Oy	325	acgggaagccagagattgtagatctcagcaaacctgcgcagtgattgaattctgycgcac	384
Db	307	ACGGGTACACCAAGATTTGTTGTTCTCAGCAAGACGACGAGTGTGAACGTTGGCGCAC	248
Oy	385	ctgtgtcatacaactgtttgcctgcgaagctgtgcgaataacataaacaagacagatga	444
Db	247	TCAGGTGCATTAACCGTTTGCTTCTGTGAGTTGCCGGGCAACAATCATGATGCTACTGCTGA	188
Oy	445	attctctgcagtgaggactggtatttcgtaacaacacatcattatgccc	491
Db	187	ATTCTGAATTGGACATGGTTCTTCATATGTCACCAATTCATTGCTC	141
RESULT	14		
LOCUS	AL385107/c		
DEFINITION	AL385107	459 bp	mRNA
ACCESSION	AL385107		linear
KEYWORDS	AL385107.1	GI:9684858	EST 03-AUG-2000
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	1 (bases 1 to 459)		
AUTHORS	Journet,E.P., Crespeau,H., van Tuinen,D., Gouzy,J., Jallou,O., Nibbel,A., Carreau,V., Chataigner,O., Kahn,D., Glanmazzi-Pearson,V. and Gamas,P.		
TITLE	Medicago truncatula ESTs from endomycorrhizal roots		
JOURNAL	unpublished (2000)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Molculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : ht-est@toulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).		
FEATURES	location/Qualifiers		
SOURCE	1..459		
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	/cultivar="Jemalong"		
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	/clone="MEBC26D07"		
	/clone_lib="MEBC"		
	/tissue_type="arbuscular mycorrhiza"		
	/dev_stage="harvested 3 weeks post inoculation with Glomus intraradices"		
	/note="Vector: pBluescript PSK. Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epilobes soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using GigaPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExSact helper phage and propagated in S01R cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of		

BASE COUNT	150 a	88 c	91 g	130 t
ORIGIN	fungal origin."			
Query Match	16.5%; Score 141; DB 9; Length 459;			
Best Local Similarity	61.5%; Pred. No. 2.2e-14;			
Matches 244; Conservative 0; Mismatches 150; Indels 3; Gaps 1;				
QY	251	taaaaggaagccatctcaaaagtctctctccgcgcagcaactctccctctgacaattgt	310	
DB	397	TATAGTGCTATGGCTATGTAAGCTAGCCTCTTCTTGACGCGGTTTCTCTGAGCATTGA	338	
QY	311	agaagaatcgcggccacgggaagccgagattgtagatctcaagcaactcgcgagttgtga	370	
DB	337	AGTAACAGCAGCAACAGGAGACCAAGATCATCTTGGAAGCAAAATTTGGAGTGTGGA	278	
QY	371	agttcggcgcaacctgg---tgataactgtttgcctgcgaagctgtgaaacaata	427	
DB	277	AGTAATCCCTTGAGAGATGGTATGCTGTCACTGATTCCTATTCTTTGTTGANTGAA	218	
QY	428	taaacacgacacgatgaattcctgcgagtggaactgtgaatttcgttaacacaactcat	487	
DB	217	CAACAGCAACCTGTGTATACCTATATTGGCTTTGGATGTTCATAGCTCACTACTTCTT	158	
QY	488	tgccaaagctgttcctcaattgttagcaggatatacagtcacaaccaatgtagatatctc	547	
DB	157	TCCCAAACTGAGCATCTGTTGTCAGGAAATATGTGCACATCACTGCAAGTGTCTC	98	
QY	548	ggaagtgagaggttgttagagactgtggaactcgtgtgcacataacaaagtatagaagt	607	
DB	97	TTAGATTAAAGATCACTAAGGCCAGGAACATCAGGGTCTGTCTACCACTGATTAAGAGG	38	
QY	608	tccttagagctctctccaccacaactcaactctgtgctt	644	
DB	37	ACCTCATGTCAACACCATCAATCTCAACTTTGGGTTT	1	
RESULT 15	BE319228	432 bp	mrna	linear EST 20-DEC-2000
LOCUS	BE319228/c	NP015088R1P1055	Developing root	Medicago truncatula cDNA clone
DEFINITION	NE015088R1	5', mRNA sequence.		
ACCESSION	BE319228			
VERSION	BE319228.2	GI:11928492		
KEYWORDS	EST.			
SOURCE	barrel medic.			
ORGANISM	Medicago truncatula			
	Euarvota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;			
	Medicago.			
REFERENCE	1 (bases 1 to 432)			
AUTHORS	Watson,B.S., Shih,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,			
	Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May			
	,G.D. and Paiva,N.T.			
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation			
	Medicago truncatula root library			
	unpublished (2000)			
JOURNAL	On Jul 14, 2000 this sequence version replaced gi:1913029.			
COMMENT	Contact: Paiva NL			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA			
	Tel: 580 221 7317			
	Fax: 580 221 7360			
	Email: nlpaiva@noble.org			
	Medicago Genome Initiative accession: MGI:S:16324			
	Insert Length: 751 Std Error: 0.00			
	Plate: 015 row: E column: 08			
FEATURES	Seq primer: TCACACAGGAACAGCTATGAC.			
source	Location/Qualifiers			
	1..432			

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/clone="NF015E08RT"
/clone_lib="Developing root"
/tissue_type="root"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Total RNA was extracted from
non-nodulated roots of plants grown in 1 mM nitrate
medium. Samples were taken at four time points
(approximately two days, one, two and six weeks post
germination) representing early seedling growth to
nitrogen limitation."
BASE COUNT      126 a      85 c      88 g      133 t
ORIGIN

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Query Match      16.4%; Score 140.8; DB 10; Length 432;
Best Local Similarity 61.4%; Pred. No. 2.5e-14;
Matches 226; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY  429 aaacagacagatgaatcctctgagtgagacttgatcttcgtaacacacacatcalt 488
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DB  426 AACACAAACCTGTGTATACCTATATTGGCTTGTGTATCTCATAGCTCATCTTCTTT 367

QY  489 gccaaaggttgctcagtgtagcagagatacagtcaccaaccaatggagatctcgcg 548
    || || | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  366 CCCAATGTAGCATCTGTGTCCAGGAATATCTGTCAATTCAGTGCAGTGTCTCT 307

QY  549 gagtgagaggttgtagagacttgagacalcctgataccataaccaagtagaagtt 608
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DB  306 TAGATTAAGGATCTAGGCCAGGAACATCAGGGTCTGTATCACCAGTGTATAGAGGA 247

QY  609 cctgaggtctctccaccaatcacaactcttgcttgcttgtaacctgagaagccttag 668
    || | || | | | | | | | | | | | | | | | | | | | | | | | | |
DB  246 CCTCATGTACACCATCATCTCAACTTGGGTTTGGTGTGATAGTGCAGGGAANA 187

QY  669 atccaagcattagtcacctctctcttgccataaagtaaccttagatgattcatt 728
    || || || || | | | | | | | | | | | | | | | | | | | | | | |
DB  186 CTCATGGCCATTGAAGACTTGTCTTGTGTACTCACAGTCATTTTCATGCTGTGGT 127

QY  729 aaacgatacaagaagctctccacaacactctgactactataaagaggtctctatat 788
    || | || || || || || || || || || || || || || || || || || ||
DB  126 AAAGAAATCAAGAACTTCTCTTATCAGCTCTTCCAAACAATGAGTGGTCTTGAGACATTCT 67

QY  789 agaatct 796
    | || | |
DB  66 TGCCATT 59

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Search completed: September 14, 2002, 18:25:04
 Job time: 23469 sec

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Db	421	aacaaataaacaacgaacagatgaatctctcagtcgaggttgaatttcgtlaaacacaa	480
Qy	481	atctatgtccaaaggttgttccacgttgttagcagggtatatacgttaaccaacaatgagga	540
Db	481	atctatgtccaaaggttgttccacgttgttagcagggtatatacgttaaccaacaatgagga	540
Qy	541	tattctcgaggtgtaggggttcgtcgtgagcttggagacatctgatactcaacaataacga	600
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Qy	601	tagaagttccctgaggtctcttccacaaatctcaactcttggcttgttttgaacctgagaa	660
Db	601	tagaagttccctgaggtctcttccacaaatctcaactcttggcttgttttgaacctgagaa	660
Qy	661	ggccttgaatcccaagccatgtatgttaactctctcttcttgccaataagtaacctttgagt	720
Db	661	ggccttgaatcccaagccatgtatgttaactctctcttcttgccaataagtaacctttgagt	720
Qy	721	gactcatcaaacggatacaagaagcttccacaacactcgttactataagtaggtctctt	780
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Qy	781	atattatagacatcttgaatcttgaacaaacctcgttgtaatttccttcgaacccggggg	840
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Qy	841	atccactagttctaga	856
Db	841	atccactagttctaga	856
RESULT 2			
US-09-060-726a-1/c			
Sequence 1, Application US/09060726a			
Patent No. 6225530			
GENERAL INFORMATION:			
APPLICANT: Weigel, Detlef			
APPLICANT: Saik Institute			
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY			
MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT			
FILE REFERENCE: SALKINS.026A			
CURRENT APPLICATION NUMBER: US/09/060,726A			
CURRENT FILING DATE: 1998-04-15			
NUMBER OF SEQ ID NOS: 13			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 1			
LENGTH: 855			
TYPE: DNA			
ORGANISM: Arabidopsis thaliana			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (63)...(590)			
US-09-060-726a-1			

[illegible]

Db	735	TTATTACACACTTATATTTGACTACTATGCGATCATCACCCTGGTTACTCGTATCA	67/6
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Db	675	TAAATGGTTTATTAATTAAAAATCTATAGATGCATTAATCTCATCGAGATGCAATAT	61/6
Oy	241	caattggttataaagaagaagacatctaaagtcttcttcctccgagccaaactctccctc	30/00
Db	615	C-ATTGGTTATTAAGAAAGAAAGCACTCAAAAGTCTTCTCTCCGCGACCACTCTCCCTC	55/7
Oy	301	tgacaattgtagaaactcgcgcgcacagggagagccgagatgtlatgaltctcagcaaatcg	36/0
Db	556	TGCACATTGTAGAAACATCGCGCCACGGGGAAGGGCGAGATTGTAGATCTCAGCAAACTCG	49/7
Oy	361	cgagtgttgaagatcttgcgcgccacctggtgcatacaactgtttgcctgcgaagtctcga	42/0
Db	496	CGAGTGTGAGTTCTTGCGCGCACCCCTGGTGCATACACTGTTTCCGCCAAGCTGTCGA	437/7
Oy	421	aacaaataaaacaacacacacgtgaatctcgcagttgagacttgaatttcgttaaacaca	48/0
Db	436	AACCATATTAACACGACACGATGAAATTCCTCTCAGTGGGACTTGGATTTTGTATACACACA	377/7
Oy	481	atcattctgcacaaggttgtctccagtttgaagaggaatcatgctaccacaaaccaatvgaga	54/0
Db	376	ATCTCATGGCCAAAGGTGTGTTCCAGTTGTACAGAGGATATCATGACCAACCAATGSGA	317/1
Oy	541	tattctcgaggttgaaggttgcctgagacttggaaacatctgatatccaccataaacaaagta	60/0
Db	316	TATTTCTGGAGGTGGGGTTCCTAGGAGTTGGAACTCTGGATCCACCATTAACCAAAAGTA	257/7
Oy	601	tagaagcttcctgaaggtctctcccaaccaatctcaaacctcttgctgttcttgaacctgaa	66/0
Db	256	TGAGAGTTCCTGAGGTCTTCTCCACCAATCTCAACTCTGTGGCTTGTTTAACCTGAGAA	197/7
Oy	661	ggccttagatccaaagcaatagtcacactctctcttggccataaglaaccttagagtgatc	72/0
Db	196	GGCCCTTAGATCCAAACCCATTAGTACCTCTTGGCCATTAAGTAACCTTTAGAGTGATT	137/7
Oy	721	gactcattaaacaggtacaaagactctcccaacaactctgacttaactataaagaggtctct	78/0
Db	136	GATCTATTAACGGATCAAGAACGTCTCCAAACAACCTGCTTACTATTAAGAGGCTCTTT	77/7
Oy	781	atattatagacatcttgcacttgaacaaacctgctgtgtaaltctctgcagcccgagg	84/0
Db	76	ATATTATAGACATCTTGATCTTGAAACAACCTCGTGCTAATTTCTCGAGCCCGGGG	17/7
Oy	841	atccactagctctcga 85/6	
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1      RESULT      3
2      US-07-644-372-1/C
3      ; Sequence 1, Application US/07644372
4      ; Patent No. 3416009
5      ;
6      GENERAL INFORMATION:
7      ;
8      APPLICANT:  Lazzeri, Mario E.
9      ;
10     APPLICANT:  Nutman, Thomas B.
11     ;
12     APPLICANT:  Weiss, Niklaus
13     ;
14     TITLE OF INVENTION:  A DNA SEGMENT ENCODING A SPECIFIC
15     ;
16     TITLE OF INVENTION:  IMMUNODIAGNOSTIC ANTIGEN
17     ;
18     NUMBER OF SEQUENCES:  2
19     ;
20     CORRESPONDENCE ADDRESS:
21     ;
22     ADDRESSEE:  CUSHMAN, DARBY & CUSHMAN
23     ;
24     STREET:  1615 L. Street, N.W.
25     ;
26     CITY:  Washington
27     ;
28     STATE:  D.C.
29     ;
30     COUNTRY:  USA
31     ;
32     ZIP:  20036
33     ;
34     COMPUTER READABLE FORM:
35     ;
36     MEDIUM TYPE:  Floppy disk
37     ;
38     COMPUTER:  IBM PC compatible
39     ;

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CORRESPONDENCE ADDRESS:
ADDRESSSEE: STERNF, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-948A-3

Query Match          5.5%; Score 47; DB 2; Length 2185;
Best Local Similarity 90.9%; Pred.No. 0.0022;
Matches   50; Conservative 0; Mismatches 5; Indels 0; Gaps 0

Dn    2018 CTCAACCCCAACCGTCGCGGAATTCCTGCAGCCGGGCGGATCACAATTCTTAGA 2072
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Qy    802 cttagacaacactgctgtcgaattccctgcagccggggagatccactagtcttaga 856
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT           5
US-08-467-947A-3
Sequence 3, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENITZ, REINER
APPLICANT: BULTZ, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
TITLE OF INVENTION: Polynucleotides Encoding Human G-protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSSEE: STERNF, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE

```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,443B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary L.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303 863-9700
TELEFAX: 303 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base.pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-443B-60

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Query Match Similarity      5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity      73.2%; Pred. No. 0.0011;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0

QY 775 tctctatatatagaacatcttgatcttgacaaacctcgtgcgaattctgcagcc 834
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 129 TATCTTGTAAAGTAGAGCGGCTCATTCACCAACCAACGCTCGTGGCGAFTCTCTGACGC 70
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 835 cgggggattccactagttcttaga 856
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 69 CGGGGATCCACTACTACTAG 48

RESULT 13
US-08-639-075A-60/c
: Sequence 60, Application US/08639075A
: Patent No. 6150125

: GENERAL INFORMATION:
: APPLICANT: Griewe, Robert B.
: APPLICANT: Rushlow, Keith E.
: APPLICANT: Wu Hunter, Shirley
: APPLICANT: Frank, Glenn R.
: APPLICANT: Stiegler, Gary
: APPLICANT: Gaines, Patrick J.
: APPLICANT: Silver, Gary
: TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
: TITLE OF INVENTION: MOLECULES AND USES THEREOF
: NUMBER OF SEQUENCES: 190
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sheridan Ross & McIntosh
: STREET: 1700 Lincoln Street, Suite 3500
: CITY: Denver
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80203
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639, 075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-639-075A-60

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Query Match          5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0011;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0

QY 775 tctctatatatagacatcttgacctggaacaacctgltgtgaattcctcgacc 834
      | ||||| ||||| | ||| || ||||| ||||| ||||| |||||
Db 129 TATCTTGTAAAGATGAGACGGCGTCATCAACCAACGCCTGTCGGAATTCTCGAGCC 70
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 835 cgggggatccactagtcttaga 856
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 69 CGGGGATCACAATACTCTAGA 48
      ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 14
US-09-012-431-60/C
Sequence 60, Application US/09012431
Patent No. 6180383
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
           Rushlow, Keith E.
           Wu Hunter, Shirley
           Frank, Glenn R.
           Stiegler, Gary
           Gaines, Patrick J.
           Silver, Gary

TITLE OF INVENTION: ELEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESS: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075

```


XX MPI: 1999-611305/52.
DR P-PSDB: AAY49098.
XX
FT New flowering locus T polypeptide that regulates flowering time,
FT particularly used to accelerate flowering -
XX
PS
XX Claim 5: Fig 2: 64pp; English.
CC
CC This sequence is the flowering locus T (FT) gene of *Arabidopsis thaliana*
CC FT regulates flowering in plants by modulating flowering time.
CC Overexpression of FT results in early flowering, while loss of function
CC mutations or antisense directed to FT causes late flowering. The FT
CC polypeptide has a molecular weight of approximately 20kD, and is located
CC on chromosome 1. The FT polypeptide is used in the invention to modulate
CC flowering time in many mono and di-cotyledonous plants. The FT
CC polynucleotide sequence is used for recombinant production of the
CC polypeptide, and as a source of antisense, ribozyme or triplex forming
CC sequences. The FT polypeptide can also be used to raise antibodies and to
CC screen for modulators or cellular binding proteins. The methods of the
CC invention allow for the production of crops at any time of year.
XX
XX Sequence 856 BP: 263 A; 150 C; 194 G; 249 T; 0 other;

Query Match	100.0%;	Score 856;	DB 290;	Length 856;
Best Local Similarity	100.0%;	Pred. No. 2,9e-190;		
Matches	856;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
Oy	1	ctcgagttctttttttttttttttttttttttataataataacacttcattcattgataataa	60	
Db	856	CTCGAGTTTTTTTTTTTTTTTTTTTAAATAATTAACACTTCATTTCATGTGATTAATA	797	
Oy	61	taattatcgatcacagaciatataaagtaaaacacttcattcttcctccctcattt	120	
Db	796	TAATTATCGATCACACACTATATAGTAAGTAAGTAACACTTCATTTCTCCCTTCATTT	737	
Oy	121	ttatfacacacttataataltgaacactactaagaacatcaacacggttcgttactgatala	180	
Db	736	TTATATACACACTTATATATTGTGAAGTAAGTATAGGCATCACCGTTCGTTACTCGATCA	677	
Oy	181	taaaatggtttttaataataaatactatagatagacaaatccatccacagatgtgaatat	240	
Db	676	TAAATATGGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	617	
Oy	241	caattggtctataaaggaagaagcaatcaaaagttcttccctcccgacacactctccctc	300	
Db	616	CAATTGGTTATTAAGGAAGTAAGAACCATCTAATGTCCTTCCTCCGACGACACTTCCTTC	557	
Oy	301	tgcacaattgttgaabaacatgcgcgcacgggaagccgagatgtgatacttcagcaaatctg	360	
Db	556	TGACAAATTTGTGAATAACATCGCGGCCACGGGAAAGCCGAGATTGTAAATCTCACCAAACTCG	497	
Oy	361	cgagttgtgaagttcttcgcgccacccctggtgatacaacatglttgcctgcgcaagctgtcga	420	
Db	496	CGAGTGTGAAGTTCTTGCGGCCACCCCTGGTCATACATGTTTGGCTGCGCAAGCTGTGCA	437	
Oy	421	aacaaataaacaacagacacagatgaaatctcctcagttgggaacttggatlttcgtaaacaca	480	
Db	436	AACAAATATAAACAACACACAGATGAATTTCTCGAGTGGGACTTGGATTTTCGTAAACACACA	377	
Oy	481	atcctatctgcacaaggttgccttcagtttgcaggtatagacaggaatacaagtaaccaaatctggaga	540	
Db	376	ATCTATTTGCCAAGAGTTGTTCCATTTGTAGCAGGAGATTCAGTCAACCAACCAATGGAGA	317	
Oy	541	tattctcgaggttgaagglttcgttagagacttggaaacatctgataccaaccaaaagta	600	
Db	316	TATTTCTCGAGAGTGAAGGTTGCTGTAGAGACTTGGAAATCTGATCTCAACCATTAACCAAGTA	257	
Oy	601	tagaagttctcctbaggatcttctccacaacatctcaactcttggtttttagaaccttgagaga	660	
Db	256	TAGAAGTTCTCGAGGTTCTTCTCACCAATCTCAACTCTTGCTTGTTTGAACCTGTAGGA	197	

[illegible]

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RESULT      2
AAZ28491
ID  AAZ28491 standard; cDNA, 856 BP.
XX
XX AC  AAZ28491;
XX
XX DT  17-JAN-2000 (first entry)
XX
XX DE  Flowering locus T (FT) gene antisense insert.
XX
XX KW  Flowering locus T gene; FT; flowering time; modulator; early flowering;
XX antibody; cellular binding protein; crop; antisense construct; ss.
XX
XX OS  Arabidopsis thaliana.
XX
XX PN  W09953070-A1.
XX
XX PD  21-OCT-1999.
XX
XX PF  13-APR-1999; 99MO-US08151.
XX
XX PR  15-APR-1998; 98US-0060726.
XX
XX PA  (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX WE  Weigel D;
XX
XX DR  WPI: 1999-611305/52.
XX
XX PT  New flowering locus T polypeptide that regulates flowering time,
XX particularly used to accelerate flowering -
XX
XX PS  Example 2; Fig 3; 64pp; English.
XX
XX CC  This is the flowering locus T (FT) gene antisense polynucleotide
XX sequence. This sequence is used in the production of the antisense
XX construct of the invention psK1060. FT regulates flowering in plants by
XX modulating flowering time. Overexpression of FT results in early
XX flowering, while loss of function mutations or antisense directed to FT
XX causes late flowering. The FT polypeptide has a molecular weight of
XX approximately 20kD, and is located on chromosome 1. The FT polypeptide is
XX used in the invention to modulate flowering time in many mono and
XX di-cotyledonous plants. The FT polynucleotide sequence is used for
XX recombinant production of the polypeptide, and as a source of antisense,
XX ribozyme or triplex forming sequences. The FT polypeptide can also be
XX used to raise antibodies and to screen for modulators or cellular binding
XX proteins. The methods of the invention allow for the production of crops
XX at any time of year.
XX
XX SQ  Sequence 856 BP; 249 A; 194 C; 150 G; 263 T; 0 other;

Query Match      100.0%; Score 856; DB 20; Length 856;
Best Local Similarity 100.0%; Pred. No. 2,9e-190;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ctcgagttttttttttttttttttttttaataataacacttcatlctcatgtagataata 60
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Db 1 ctcgagttttttttttttttttttttttaataataacacttcatlctcatgtagataata 60
QY 61 taattatcgatcacacacatatataagtaaaacacttcatlctctccctctcatl 120
|||
Db 61 taattatcgatcacacacatatataagtaaaacacttcatlctctccctctcatl 120
QY 121 ttatttaacacttaattatgaactatagatagacatcacggttgatctgata 180
|||
Db 121 ttatttaacacttaattatgaactatagatagacatcacggttgatctgata 180
QY 181 taaaatggttataataataataataataataataataataataataataataata 240
|||
Db 181 taaaatggttataataataataataataataataataataataataataataata 240
QY 241 caattggttataaagaagaagacatctaaagtcttctctccgcagccactctc 300
|||
Db 241 caattggttataaagaagaagacatctaaagtcttctctccgcagccactctc 300
QY 301 tgaacaattgtagaanaacttgcgcgcagccggaagcgagattgtagatctcagaactcg 360
|||
Db 301 tgaacaattgtagaanaacttgcgcgcagccggaagcgagattgtagatctcagaactcg 360
QY 361 cgaagtgttgaagtcctgctgcgcacccctggtgcatacactgttgcctgcagagtcgca 420
|||
Db 361 cgaagtgttgaagtcctgctgcgcacccctggtgcatacactgttgcctgcagagtcgca 420
QY 421 aacaaataaacaacgacagatgaattccctgcagtgtagaacttgatatttgtaacaca 480
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Db 421 aacaaataaacaacgacagatgaattccctgcagtgtagaacttgatatttgtaacaca 480
QY 481 atctcatgtccaaaggttgcctcagttgtagcagggatatacagtcacacaaacttgagaa 540
|||
Db 481 atctcatgtccaaaggttgcctcagttgtagcagggatatacagtcacacaaacttgagaa 540
QY 541 tatctcgcagagtgtagaggttgcctcagttgtagaacttgatatttgtaacaca 600
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Db 541 tatctcgcagagtgtagaggttgcctcagttgtagaacttgatatttgtaacaca 600
QY 601 tagaagttcctcgaaggttgcctcagttgtagaacttgatatttgtaacaca 660
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Db 601 tagaagttcctcgaaggttgcctcagttgtagaacttgatatttgtaacaca 660
QY 661 ggccttagatccaaagcattatgacacttctcttgccataagaactttagagtgat 720
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Db 661 ggccttagatccaaagcattatgacacttctcttgccataagaactttagagtgat 720
QY 721 gatctatataacgagatcaagaacgctctccaaacactctgcttactataagaaggctct 780
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Db 721 gatctatataacgagatcaagaacgctctccaaacactctgcttactataagaaggctct 780
QY 781 atatttataacatcttgccttgtaacaaacactcgtgtaacttctcgcagcccgagg 840
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Db 781 atatttataacatcttgccttgtaacaaacactcgtgtaacttctcgcagcccgagg 840
QY 841 atccactagttctaga 856
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Db 841 atccactagttctaga 856

KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EPI033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 07-MAY-1999; 99US-0132486.
PR 11-MAY-1999; 99US-0132487.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
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PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144088.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
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PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145919.
PR 27-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 03-AUG-1999; 99US-0146388.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 80.9%; Score 692.4; DB 21; Length 775;
Best Local Similarity 99.9%; Pred. No. 4e-152;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 119 ttltatcacactatataatgaactactataggcatcatcaacggttcgltactcglat 178
DB 758 ttt 699
OY 179 cataaatggttataataataataatcatalagatgcataaatcatalaagatgat 238
DB 698 CATTAATGTTATTATAATTAATAATCTATGATCATTAATCTATGATGATGAT 639
OY 239 atcaatlggtlataaaggaaagccatcaaatgctctctctccgagccactctcc 298
DB 698 ATCAATTTGGTTATAAGGAAGACCATCTAAGCTCTTCTCTCCGACGACCTGCC 579
OY 299 tctgacaattgtagaaactgcgcacgaggaagcgagattgtagatctcaagaact 358
DB 578 TCTGACAAATTTGAGAAACTCGCGCCACGCGGAGGACGAGATTGATCTTCAGCAACT 519
OY 339 cgcgagtgtagaagttcggcgccaccctgltgcatlacacglttgctgcgaagcttc 418
DB 518 CGCGAGTGTGAAGTTCTGGCGCCCTGTGCTATACCTGTTGCTCCCAAGCTGTG 459
OY 419 gaaacaataaacaacgacatgaattcctgcagtggaacttgatcttcgataacaca 478
DB 458 GAACCAATATAACACGACGATGATTTCTCGAGTGGAGCTTGATTTTCGTATACACA 399

Qy 479 caatcctatgccaaggltgtccagltgtagcaggatatacagtcaccaaccaatgga 538
|||||
Db 398 CAATCTATTCGCAAGGTTGTTCAGTGTAGCAGGAGATATCAATCAACCAATGGA 339
Qy 539 gatattcgcgaagtggaaggtgtcgaagcttggaacatctggaatccacataacaaag 598
|||||
Db 338 GATATTCGAGGAGGAGGTTGCTAGAGACTTGGAACTATGATCCACCAATAAACCAAG 279
Qy 599 tatagaattccttagagctctccacaatctcaactctggtgtgtttgaacctag 658
|||||
Db 278 TATGAAGTTCTCTGAGGTTCTCCACCAATCTCAACTCTGGCTGTGTTTGAACCTGAG 219
Qy 659 aaggccttagatccaagccattagtcacactcctcttggcataaagtaaccttaagtcga 718
|||||
Db 218 AAGGCTTAGATCCAAAGCCATTAGTCACCTCTTGGCCATAAATACCTTTAGATGA 159
Qy 719 ttgatctatataaggaatcaagaacggtccacaacactctgcttacttaagaaggtctc 778
|||||
Db 158 TTGATCTATTAAACGAGATCAAGAACGTCCTCCAAACAACCTGCTTACTATAGAGGCTCTC 99
Qy 779 ttatattatagacactcttgatcttgagacaac 812
|||||
Db 98 TTATATTATAGACATCTTTCATCTTGAACAAC 65

RESULT 4
AAC48359/c
ID AAC48359 standard; DNA: 754 BP.
XX

AC AAC48359;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123160.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140921.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144684.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147302.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148365.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.

PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 80.8%; Score 692; DB 21; Length 754;
 Best Local Similarity 100.0%; Pred. No. 4,9e-152;
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 ttatcacactatataattgaactaiaagacatcacacgttcgttactgtatca 180
 |||||||
 DB 754 TTATTACACACTTATATATTTGAATCTATAGCATCAATCAATCAATCAAT 695
 QY 181 taaatggttataaataataactatagatgacataatccatcagatgtgaaat 240
 |||||||
 DB 694 TAAATGGTTATTAATAATAATTAATTAATTAATTAATTAATTAATTAATTA 635
 QY 241 caattggtataaagaagaagccatctaaagtcctctcctccgacgcactccctc 300
 |||||||
 DB 634 CAATTGGTTATTAAGGAAGAACCAATCTAAAGTCTTCTCCCGCAGCACTTCCCT 575
 QY 301 tgacaattgtagaaaactgcygcacaggaagccgagatgttagatctcagaaactcg 360
 |||||||
 DB 574 TGACAAATTTAGAAAACCTCGCGCCACGGGAGCGAGATTTGATATCTACACAACTCG 515
 QY 361 cgaagtgtgaagttcttggcgccacccttggtagatcaacatggttgcctgcaagctgtcga 420
 |||||||
 DB 514 CGAGTGTGAAGTCTCGGGCCACCCTGTCATACACTGTTGCTTGCCTGCCAAGCTGTGCA 455
 QY 421 aacaalataaacacgacacgatgaatttcctcgagtggagcttgaatttcgtaaacaca 480
 |||||||
 DB 454 AACCAATATAAACACGACGACGATGAATTCCTCGAGTGGGACTTGATTTTCGTAACACACA 395
 QY 481 atcctatgccaaggttcttccagttgttagcaggatatacgttaaccaacaaatggaga 540
 |||||||
 DB 394 ATCTCATTTGCCAAGGTTGCTTCAGTTGTAGCAGGATATCAGTCAACCAATGGAGA 335
 QY 541 tattcctcgaggttgaggttcttgcctagacttgaacatcctggaatccacaataacaaatga 600
 |||||||
 DB 334 TATTCTCGAGGTGAGGGTTCCTAGGACTTGGAACTTGGATCCACCACTTAACCAAGTA 275
 QY 601 tagaagttcctgaggttcttccaccacatcacaactcttgctgtgtttgaacctgagaa 660
 |||||||
 DB 274 TAGAAGTTCCTGAGGCTTCTCCACCAATCTCAACTCTTGCTTGTGTAACCTGAGAA 215
 QY 661 ggccttagatccaagccatagtaacctctcttggccataagtaacctttgagtgatt 720
 |||||||
 DB 214 GGCCTTAGATCCAAAGCCATTAATCACTCTTTGGCCCTTAAGTAACCTTTAGAGTATT 155
 QY 721 gatcatiaaagatccaagaagcttccacaacaactcttaccataaagaggtctct 780
 |||||||
 DB 154 GATCTATTAAAGGATCAAGAACGCTTCCACAACACTCTCTTATAGAGAGGCTCTT 95
 QY 781 atattatagacatcttgaatcttgaacaac 812
 |||||||
 DB 94 ATATTATAGACATCTTGTGATCTTGAACAAAC 63

RESULT 5
 AAA60683/C
 ID AAA60683 standard; DNA; 528 BP.
 XX
 AC AAA60683;
 XX
 DT 26-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:2.
 XX
 KW Arabidopsis thaliana; Cruciferae; plant; control; flowering;

||||| 11 1111 11 11 111111 1111 11111111
Db CGGTGATAAACGTTGTCTTCGAGTTGGCGGAGAACATACCAACAATACGATGAT 349
QY 447 tctgcagctggagcttgatgatttcgttaacacacacatctcatgccaaggtgttcag 506
Db 348 TCCCGAGGGGGAGGTGACTCTGTGACACACCACCTCATTTGCCAAAGGCATTTCCAGT 289
QY 507 tgtacgagggatcatcagtcaccacacatgagatattctcgagagtgaggggttcag 566
Db 288 GGTGGCAGGATATCATCATCACCAACCGAGTGAGATATTCTGCTTGTTGGGCTTTGG 229
QY 567 acttggacacatctggaatccacacataacaaaglaagaagttcccttgagttctccacc 626
Db 228 ACTGGCAGCATCTGATGCCACCATTAACAGAGAGTGTAGAAATTTCTGAAGTGTCTCTCC 169
QY 627 aatctcaactcttgctgtgtttgaaacctgagaagcgcttagatccaaagcattagtcac 686
Db 168 AATCTCCACTATTGGTTGTTCAGAACTTGAGAGGCTTAGATCCAAAGCATTAAGTAAC 109
QY 687 ctctcttgagcacaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 746
Db 108 CTCTCTATGGCCATTAATGACCTTAAGAGAGACCACTCTGCTGAAGGATCAAGAACATC 49
QY 747 tccacaacactctgcttactataagaagggctctctatattatagacat 794
Db 48 TCCAAACAACACTGGCGACCAAGAGAGATCTCTACGACTTAAGACAT 1

RESULT 7
AA60684/c
ID AAA60684 standard; DNA; 528 BP.
XX
XX AAA60684;
XX
XX 26-OCT-2000 (first entry)
DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.
XX
XX Arabidopsis thaliana; Cruciferae; plant; control; flowering;
KM solar radiation; ds.
XX
XX Arabidopsis thaliana.
OS
PN JP2000139250-A.
XX
PD 23-MAY-2000.
XX
PF 11-NOV-1998; 98JP-0320219.
XX
PR 11-NOV-1998; 98JP-0320219.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2000-425906/37.
XX
XX
XX A method to accelerate plant generation and generation accelerated
PT plants -
XX
PS Claim 5; Page 5; 6pp; Japanese.
XX
XX the present invention describes a method to accelerate plant generation
CC and generation accelerated plants. The method uses a controlling gene
CC functioning in the downstream of a gene under the control of solar
CC radiation to accelerate plant generation using a gene functioning to
CC accelerate the flowering time regardless of solar radiation. The method
CC can control flowering time to a desired period by shortening the
CC juvenile stage. The present sequence represents a specifically claimed
CC Arabidopsis nucleotide sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 528 BP; 122 A; 117 C; 142 G; 147 T; 0 other;

Query Match 43.7%; Score 374.4; DB 21; Length 528;
Best Local Similarity 81.8%; Pred. No. 5.2e-78;
Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 267 cttaagttcttcctcccgagcgaacttcctctgacaattgtagaanaatcgcgccac 326
Db 528 CTACGTTCTTCTCTCCACACAGCATTTCTCCCTCGGACGTTGAAGTAAAGCAGCCAC 469
QY 327 gggagagccgagatgttagatctcagaactcgcgagttgttgaagttctggccacc 386
Db 468 AGGAAGACCAAGATTGATGATCTCAGCAAACTCAGAGTGTGAACTGTGGCCACACC 409
QY 387 tgggtcacacactgttgccgccaagctgtcgcgaacaataaacaacgacagatgaat 446
Db 408 CGGTGATAAACGTTGTCTTCCGAGTTGCCGGAACATATCCAAACATACGATGAT 349
QY 447 tctgcagctggagcttgatgatttcgttaacacacacatctcatgccaaggtgttcag 506
Db 348 TCCCGAGGGGGAGGTGACTCTGTGACACACCACTCATTTGCCAAAGGCATTTCCAGT 289
QY 507 tgtgcagagggatcatcagtcaccacacaaatgagatatctcgaggtgaggtgttcag 566
Db 288 GGTGGCAGGATATCATCATCACCAACCGAGTGAGATATTCTGTTGAGGGTTGCTTGG 229
QY 567 acttggacacatctgataccacacataacaaaglaagaagttcccttgagttctccacc 626
Db 228 ACTGGCAGCATCTGATGCCACCATTAACAGAGAGTGTAGAAATTTCTGAAGTGTCTCTCC 169
QY 627 aatctcaactcttgctgtgtttgaaacctgagaagcgcttagatccaaagcattagtcac 686
Db 168 AATCTCCACTATTGGTTGTTCAGAACTTGAGAGGCTTAGATCCAAAGCATTAAGTAAC 109
QY 687 ctctcttgagcacaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 746
Db 108 CTCTCTATGGCCATTAATGACCTTAAGAGAGACCACTCTGCTGAAGGATCAAGAACATC 49
QY 747 tccacaacactctgcttactataagaagggctctctatattatagacat 794
Db 48 TCCAAACAACACTGGCGACCAAGAGAGATCTCTACGACTTAAGACAT 1

RESULT 8
AAC90636/c
ID AAC90636 standard; cDNA; 522 BP.
XX
XX AAC90636;
XX
XX 20-MAR-2001 (first entry)
DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 5.
XX
XX Strawberry; flowering regulation; floral homeotic gene; field crop;
KM harvesting; fruit production; ss.
XX
XX Fragaria vesca.
OS
PN WO200071722-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US14297.
XX
PR 25-MAY-1999; 99US-0318789.
XX
PR 24-MAY-2000; 2000US-0318789.
XX
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
XX
PI Oeller P, Guttersen N;
XX
XX WPI; 2001-025165/03.
DR P-PSDB; AAB50266.
XX
XX Novel nucleic acid involved in controlling plant flowering processes is

PT useful for generating transgenic plants, in particular strawberry
PT plants having altered flowering behavior such as early, delayed or
PT day-neutral flowering

PS Claim 3; Page 59-60; 97pp; English.

CC The present invention provides the nucleic acid and protein sequences of
CC a number of proteins from the strawberry which are involved in the
CC regulation of flowering. These were identified using primers based on the
CC homologous sequences from *A. thaliana*, *B. napus* and *R. sativus*. They can
CC be used in the production of transgenic field crops whose flowering is
CC regulated and the time of fruiting and harvesting can be manipulated.

XX Sequence 522 BP; 147 A; 111 C; 129 G; 135 T; 0 other;

Query Match 21.1%; Score 180.2; DB 22; Length 522;
Best Local Similarity 60.8%; Pred. No. 1e-32;
Matches 312; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

QY 277 ctctccgcagcagcactctccctctgacaattgtagaacaaactcgagcgaggaagcg 336
DB 518 COTCTTCTTGACAGAGTTCCCTGTGGCATTGAGAGACAGACGCCAGGAGCCCG 459
QY 337 agatgtgacatcagcaactcgagagtgtgaagctctgagcgccaccctggtgcatc 396
DB 458 AACTCGTTTGTTCGCAAACTTTCGACTGCGAATGTCCTTGAAGAGAGGAATC 399
QY 397 actgtctgcagcagagctgcaacataataacacagacagatgaattcctgcaagt 456
DB 398 ACTGCTCTGCTTACTTCTTCTTGTGAACAAGAGAACACAAACCTGTGATCCTTATGTT 339
QY 457 ggaactgtgatttcglaaacacaaatcctcaatgccaagtggtcagttgtagcaagg 516
DB 338 GGCCTCGGCATTTCATATTTACCCACCTCCCTCCAAATGTCGATGTCGTTCTCTGGG 279
QY 517 atatagtcaccacaactatgagatatctcggagtgagggtgtcaggctgaggaaca 576
DB 278 ATGTCCGAGACTATCCAGTGCAGAGTCCTTCAGGTAAAGATGTCATCTGAGACCTGGAACA 219
QY 577 tctgataccacatacaagaatataagaagtcctgaggtctctccccaactcacaact 636
DB 218 TCTGGGTACATCATACCAAGTGTAAAGAAAGATCTCATATCCCTCCATGAACTTCAAC 159
QY 637 ctgtgctgttcttgaacctggaagccttagatcacaagcattagtcac---ctctct 693
DB 158 TTAGGCTTGAGCGGTACAGAGGAAGATATAGCTCATGTATACACCTTTTGGCTG 99
QY 694 tggcacaatgaaccttagagtgatgtatcattataaaccgagtaagaagctcaca 753
DB 98 GAGTTGTAAAGTCACTGTCAATTTTAACACTGGGTGGAACAACATTAACATCTCCAAATG 39
QY 754 actcgtctactataagaaggtccttataatt 786
DB 38 ACTCTTCCAACACAAAGAGATCTGAGATCTTT 6

RESULT 9
AAT60140/C
ID AAT60140 standard; cDNA: 668 BP.
XX AAT60140;
AC
XX 24-JUN-1997 (first entry)
DT
XX
DE Arabidopsis terminal flower1 (tfl1) cDNA.
XX
XX Terminal flower 1; tfl1; centroradialis; cen gene; flowering;
KW transgenic plant; ss.
XX
XX Arabidopsis thaliana var. Columbia.
OS
XX
FH Key Location/Qualifiers

FT CDS 16..549
FT /*tag= a
FT mutation 221
FT /*tag= b
FT /*note= "tfl1-14 allele has T at position 221"
FT mutation 274
FT /*tag= c
FT /*note= "tfl1-13 allele has G at position 274"
FT mutation 307
FT /*tag= d
FT /*note= "tfl1-11 allele has G at position 307"
FT mutation 329
FT /*tag= e
FT /*note= "tfl1-1 allele has G at position 329"
XX
XX W09710339-A1.
XX 20-MAR-1997.
XX 13-SEP-1996; 96WO-GB02276.
XX 13-SEP-1995; 95GB-0018731.
XX (INNE-) INNES CENT JOHN.
XX Bradley DJ, Carpenter R, Coen ES;
XX WPI: 1997-202235/18.
XX P-PSDB; AAM13945.
DR Antirrhinum majus centroradialis gene and Arabidopsis homologue,
PT tfl1 - control switching of apical meristem to floral fate, useful
PT in plant hybridisation and in control of growing season
PS Claim 12; Fig 6a; 83pp; English.
XX
XX A cDNA clone (AAT60140) codes for the terminal flower1 (TFL1) protein
CC (AAM13945) of Arabidopsis thaliana. It was obt. from an Arabidopsis
CC expressed sequence tag, clone 129D77. A genomic tfl1 clone
CC (AAT60142) has also been obt. The wild-type role of the tfl1 gene
CC is to inhibit flowering and to prevent the apical meristem from
CC switching to a floral fate. The tfl1 gene was identified as a
CC homologue of the Antirrhinum centroradialis gene (see also AAT60141).
CC The flowering characteristics of transgenic plants, esp. switching
CC of apical meristem to a floral fate and the timing of flowering,
CC can be manipulated by regulating cen or tfl1 gene expression.
XX
XX Sequence 668 BP; 195 A; 135 C; 147 G; 191 T; 0 other;

Query Match 20.7%; Score 176.8; DB 18; Length 668;
Best Local Similarity 60.6%; Pred. No. 5.7e-32;
Matches 308; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY 293 tctcccttgacaattgtagaacaaactcgagcgaggaagcggagatgtgatactcag 352
DB 529 TTTCTCTTGTGCGTTAAAGAGACGCCGACAGGAGACCAAGATCATACCTGCACG 470
QY 353 caaactcgagagtggtgaagttctggcgcaaccctggtc---gcataactgttcctgc 409
DB 469 CAATTTTACGAGTGTGGAAGTATCTCTCGAAGGAGATTTAGGAAGATTAACACGCTTT 410
QY 410 caagctgcgaacacataaacaacagacagatgaattcctgcagtgaggacttgatttc 469
DB 409 GCTTCTGCCTGANAAGAACAAACAAACATATGATCCCTATGCTTGCCCTTGCAATT 350
QY 470 cgtaacacacaatcctcatcgaagagtggtcagagttgtagcagagatcagtcacca 529
DB 349 CATAGCTCACACACCTCTTGGCCAAACGTAGCATCTGTTGTGCGGGAATGTTTGAACA 290
QY 530 accaatgagatattctcgcgagtgaggtgtgctgagacttgaaacttgatcacca 589
DB 289 TCCAGTGCAGGTGTTCTTTTGAAGAGGCTACTAGGACCTGGAACATCTGGGCTATCA 230

QY 590 taaccaaagatagaagttcctcctgaggtctccacccaatcacaactcttgctgtttt 649
 Db 229 TCACCAAGATGAAGAGATCTGAGATCACCACCATGGATCTCAACCTTAGCCTTGGAGG 170
 QY 650 gaacctgagaagcgttagatcccaagccatagtcacctctctcttgccataagtaacct 709
 Db 169 AACAGAGAAGAGAAAGAGCTCATGGCCATTGGAGACTTGGCTTGTATTAACATACAT 110
 QY 710 tttagatgatgatcatttaaacgagatcaagacgctccacaacactctgtctactataa 769
 Db 109 TCACCTTAGTGTGGAGTGAAGAAATCAAGAACATCTCTACACATCTCCCATTTATCA 50
 QY 770 gagggtcctatataatfatagacatctt 797
 Db 49 ATGGCTTATCACTCTAGTTCCTCATATT 22
 RESULT 10
 AAC90668/c
 ID AAC90668 standard; cDNA; 519 BP.
 AC AAC90668;
 XX 20-MAR-2001 (first entry)
 DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 43.
 XX Strawberry; flowering regulation; floral homeotic gene; field crop;
 KW harvesting; fruit production; ss.
 OS Fragaria vesca.
 PN W0200071722-A1.
 XX 30-NOV-2000.
 PD 24-MAY-2000; 2000MO-US14297.
 PF 25-MAY-1999; 99US-0318789.
 PR 24-MAY-2000; 2000US-0318789.
 XX (DNAP) DNA PLANT TECHNOLOGY CORP.
 PA Oeller P, Guttersen N;
 XX WPI; 2001-025165/03.
 DR P-PSDB; AAB50271.
 XX Novel nucleic acid involved in controlling plant flowering processes is
 PT useful for generating transgenic plants, in particular strawberry
 PT plants having altered flowering behavior such as early, delayed or
 PT day-neutral flowering
 XX Claim 23; Page 94-95; 97pp; English.
 PS The present invention provides the nucleic acid and protein sequences of
 CC a number of proteins from the strawberry which are involved in the
 CC regulation of flowering. These were identified using primers based on the
 CC homologous sequences from A. thaliana, B. napus and R. sativus. They can
 CC be used in the production of transgenic field crops whose flowering is
 CC regulated and the time of fruiting and harvesting can be manipulated.
 XX Sequence 519 BP; 143 A; 132 C; 120 G; 124 T; 0 other;

Query Match 18.8%; Score 161.2; DB 22; Length 519;
 Best Local Similarity 57.3%; Pred. No. 2,7e-28;
 Matches 292; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 277 ctctctcgcagcagcactctccctctgacaaltgtagaaaactcggcgcaagggaagcg 336
 Db 515 CGCTCTCTGCTGCGCTTCTCTCTGTCATTGAAGTAAACGCGACGAACAAACACCA 456

QY 337 agattgtagatctcagcaaacctcgcgagtggttgaagttctgsgcgcaacctggtgcatc 396
 Db 455 AGTGCGTTTTCGGCTGCCAAGGTTTCGGGTGTTGAGTATCCCTTGAAGGAAGGGGTTTC 396
 QY 397 actgttgcctgcgaagcgtctgcgaacaataaaacacagacagatgaattccctgcagtg 456
 Db 395 ACCGACTGCCCTTCGTTTTCATGATGAGAGAACAAACAAACCTGTGATGCTATGTTT 336
 QY 457 ggaacttgatttctgtaacacaacatctcatctgcacaaggttgctcagttgtagcagg 516
 Db 335 GGCCCTTGGCATCTGTGACTCCACCACCTTCTTCCAAATGTAGCATCTGTGGTGCACAGA 276
 QY 517 atatacagtcaccaacaatlgagatattctcggagtgtaggggttgctagagacttggaaca 576
 Db 275 ATGCTGTACAAATTCAGTGCAGGTCCTCTTCAATTAAGATCATTAAGGCCACAGACCA 216
 QY 577 tctgataccacaataacaaagatagaagttcctcgtgagttctctccaccaatcctaact 636
 Db 215 TCTGGCTGTGCATTACCAAGAGTGAAGATGATCATGTGCGCTTGTGAATGCACAACT 156
 QY 637 ctgagcttgcttgaacctgagaagccttagatccaagccatagttacctctcttg 696
 Db 155 CTAGGTTGGCGGTGACTGCAAGGGAGAGAGCATATGTCATTCACAGCAGCTTGCTG 96
 QY 697 coataagaacacttagagtgatgatcatttaaacgagatcaagaagctccacaact 756
 Db 95 TTGTAGAGACAAATCATTTTGTATGAGGGGTGAAGGATCAAGAACATCTCTATGACT 36
 QY 757 ctgcttactataaagggtctcttataatt 786
 Db 35 CTTCACACAGCTAGAGGTTCCGACATTCCT 6

RESULT 11
 AAV66749
 ID AAV66749 standard; DNA; 4512 BP.
 XX AAV66749;
 AC AAV66749;
 XX 02-FEB-1999 (first entry)
 DE Arabidopsis pathogen response gene LSD1.
 XX Arabidopsis
 KW LSD1; plant pathogen response; apoptosis; programmed cell death;
 KW disease resistance; herbicide resistance; transgenic plant;
 KW crop protection; ss.
 XX Arabidopsis thaliana.
 OS
 XX Key Location/Qualifiers
 FH 2371..3783
 FT CDS
 FT /*tag= a
 FT /*note= "contains codons"
 FT 2371..2494
 FT /*tag= b
 FT exon
 FT 2495..2583
 FT /*tag= c
 FT intron
 FT 2584..2688
 FT /*tag= d
 FT exon
 FT 2689..3177
 FT /*tag= e
 FT intron
 FT 3178..3317
 FT /*tag= f
 FT exon
 FT 3318..3417
 FT /*tag= g
 FT intron
 FT 3418..3490
 FT exon

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FT		/number= 4
FT		/transl_except= (pos:3433..3466, aa:Val)
FT		/note= "this codon has an apparent 1 nucleotide insertion, which alters the reading frame"
FT	Intron	3491..3582
FT		/tag= 1
FT		/number= 4
FT	exon	3582...3658
FT		/tag= j
FT		/number= 5
FT	Intron	3659..3746
FT		/tag= k
FT		/number= 5
FT	exon	3747..3783
FT		/tag= l
FT		/number= 6
XX		
XX		
XX		
PD	03-SEP-1998.	
XX		
PF	27-FEB-1998;	98MO-USO4077.
PR	28-FEB-1997;	97US-0039063.
XX		
PA	(UYNC-) UNIV NORTH CAROLINA.	
PI	Dangl JL, Dietrich RA, Epple PM, Richberg MH:	
XX		
DR	WPJ; 1998-531501/45,	
DR	P-PSTB; AAW72366-67.	
PT	New isolated Arabidopsis genes - useful for producing transgenic plants which show resistance to cell death caused by pathogens or herbicides.	
PS	Claum Z; Page 34-38; 88pp; English.	
CC	This is the nucleotide sequence of the wild-type LSD1 gene of Arabidopsis thaliana. It includes exons encoding an LSD1 polypeptide (see AAW72366-67) that has an effect in regulating the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. LSD1 functions to monitor levels of superoxide-dependent signal and negatively regulates a plant cell death pathway. To isolate the gene and LSD1 cDNA (see AAV66750-51), Arabidopsis mutants were obtained which exhibited constitutive cell death in the absence of pathogens. The lesion stimulating disease resistance or LSD phenotypes, which provided resistance to cell death, was then analysed by genetic CC and physical complementation studies. The sequences obtained were then compared to databases. The invention provides LSD1 CC polypeptides and isolated DNA sequences, a transformation vector, CC mutated LSD1 DNA sequences, and a transgenic plant expressing LSD1 mutant genes that affect resistance to herbicidal compounds or plant pathogens that normally result in plant cell death. Also CC claimed are LSD1-like (LSD1 and IOD2) proteins (see AAW72380-81) and CC claimeds that interact with LSD-1 (see AAW72384-96). Products of the CC invention can be used to produce plants that show resistance to cell death caused by pathogens or herbicides.	
XX		
SQ	Sequence 4512 BP; 1385 A; 819 C; 767 G; 1539 T; 2 other;	
Query Match	17.0%; Score 145.8; DB 19; Length 4512;	
Best Local Similarity	77.38; Pwd. No. 1.8e-24;	
Matches 177; Conservative	0; Mismatches 52; Indels 0; Gaps	
OY	580 ggaaccacaaacaaagataagaattctgagggtccatcacaacactcaacctt 639 	
Db	122 ggagagaagaatcaccaaagtgttagaatcttcctaagatgcgctctccaatcccatatt 181	
OY	640 agcttgctttgaacctgaagaaggctttagatccaagccattagtaaccttcttgcca 699	

[illegible]

Oy	328	ggaagggccggagatgltgatacttcgaacaaactcggagltgtgaagttcttggcgccacct	387
Db	561	GGGAGGGCCCAATTCATTTTCCGTGTCGAATTTTCTCGTTGGTAATCATCCCGACACAT	522
Oy	388	ggtgcata-----cacgtcttgcgcgaacgctgcgaacaaataataacagaca	438
Db	521	ACTGGTGGGCTCAACATTCGCGCTGCGCTTTTCTCTGTTTGAACAGCAATAATTACAAAC	462
Oy	439	cgatgaattcctgcagttggagacttggatlttcgtaacacaaatctcatgccaaagtt	498
Db	461	CTGTGGATCCCTATGTTGGGCTTGGGATCTCAATAGCTCACTCTTTTCCGGAATGAG	402
Oy	499	gttcacgtttgagagggatataagtaaccaacaaaggagatattctggaggttgaagg	558
Db	401	GAATCAGTGGTCCCTGGGATATCTGTGACTATATCCAGTGCAAAGTCTCTCCACAGTATGA	342
Oy	559	ttgcagagacttggaaacatctgataccacaataacaaaglatagaagttccttgaagttc	618
Db	341	TCACATGAGCAGGAGAACATCAGGGTCTGTGATATTCAGACGTGAATAATGATCATATCA	282
Oy	619	tctccaccaatctaactcttggcttglttgaaccctggaagcgcttaatccaagcca	678
Db	281	CCACCATCAACCTTAACCCCTTAGGTGAGAGTAACAGGAGGAAGAAAGACTCATGCGCA	222
Oy	679	ttagtcacctctcttggcca-----taagtacctttagagtgatgatcta	726
Db	221	TTGTAGACATCTGTAATGGAAATTTGTGGAGTGTGAATAATACAGACATTTTAAACAGTTGAG	162
Oy	727	ttaaacggatcaagaacgctccacaacactctgactaactataagaaggtc	776
Db	161	GTAATAATGATCAACAGCTCTCCCATATATCTCCCTTTCACATAGCGGGCT	112

RESULT 13
 AAC90666/c
 ID AAC90666 standard; DNA; 3696 BP.
 XX
 AC AAC90666;
 XX
 DT 20-MAR-2001 (first entry)
 XX
 DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 37.
 XX
 KW Strawberry; flowering regulation; floral homeotic gene; field crop;
 XX harvesting; fruit production; ds.
 XX
 OS Fragaria vesca.
 XX
 PN WO200071722-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14297.
 XX
 PR 25-MAY-1999; 99US-0318789.
 XX
 PR 24-MAY-2000; 2000US-0318789.
 XX
 PA (DNAP) DNA PLANT TECHNOLOGY CORP.
 XX
 PI Oeller P, Guttererson N;
 XX
 DR WPI: 2001-025165/03.
 XX
 DR P-PSDB; AAB50269.
 XX
 PT Novel nucleic acid involved in controlling plant flowering processes is
 XX useful for generating transgenic plants, in particular strawberry
 PT plants having altered flowering behavior such as early, delayed or
 XX day-neutral flowering
 XX
 PS Disclosure; Page 82-87; 97pp; English.
 CC
 CC The present invention provides the nucleic acid and protein sequences of
 CC a number of proteins from the strawberry which are involved in the

CC regulation of flowering. These were identified using primers based on the
CC homologous sequences from *A. thaliana*, *B. napus* and *R. sativus*. They can
CC be used in the production of transgenic field crops whose flowering is
CC regulated and the time of fruiting and harvesting can be manipulated.
xx
SQ Sequence 3696 BP; 1175 A; 618 C; 648 G; 1255 T; 0 other;

Query Match	9.6%;	Score 82.6;	DB 22;	Length 3696;
Best Local Similarity	60.4%;	Pred. No. 9.4e-10;		
Matches 136;	Conservative 0;	Mismatches 89;	Indels 0;	Gaps 0;

QY 277 cttctctccgcagcagcactctccctctgcaaatctgtgaaaacctcgcgcgcgaagccgc 336

Db 2636 CGCTCTCTTGCGAGCATGTTTCCCTCTCGGGCATTTTAAACAGACGCCACCGGAAGCCCG 2577

OY 337 agatgtgatactcagcaaacctcgcaggttgaagttctgcygcacccctggtacac 396

Db 2576 AACGCTTTGTTTCTGCAAACTTTCGACGTCTGCAAAATGGTCCCTCGAAGAGGAGGAATC 2517

OY 397 acgttttgcctgcacagctctgcgaaacatataaacagacagacagatgaattctcagtg 456

Db 2516 ACTGCTCCCTCACTTCTCTGTTGAACAAAGAACACAAACCTGTGATCTCATGTGTT 2457

OY 457 ggaacttgatatttcgtatacacacaatctcatctgcgaaagttgct 501

Db 2456 GGGCTCGGCATTTCAATTTTCACACCTCCCTTCTCGCAGATATT 2412

RESULT	14
AAT60142/c	
ID	AAT60142 standard; DNA; 1430 BP.

AC AAT60142;

DT 24-JUN-1997 (first entry)

DE *Arabidopsis* terminal flower 1 (tfl1) gene.

Terminal flower 1; *tfl1* gene; centroradialis gene; *cen* gene;

KW flowering; transgenic plant; ss.

OS *Arabidopsis thaliana* var. *columbia*.

Key	Location/Qualifiers
FH	

FT	/*tag= a
----	----------

Feature	Position (nt)
5' UTR	1-44
Exon 1	45-100
Intron 1	101-145
Exon 2	146-200
Intron 2	201-245
Exon 3	246-300
Intron 3	301-345
Exon 4	346-400
Intron 4	401-445
Exon 5	446-500
Intron 5	501-545
Exon 6	546-600
Intron 6	601-645
Exon 7	646-700
Intron 7	701-745
Exon 8	746-800
Intron 8	801-845
Exon 9	846-900
Intron 9	901-945
Exon 10	946-1000

FT	exon	656..717
1	1	656..717

FT	intron	718..923
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FT	exon	924..964
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100	100	100

FT	exon	1052..1430
1	1	1052..1430

FT /cag 3 /note= "in-frame stop codon at 1261-1263"

PN W09710339-A1

PD 20-MAR-1997.

PF 13-SEP-1996; 96WO-GB02276.

PR 13-SEP-1995; 95GB-0018731.

PA (INNE-) INNES CENT JOHN

PI Bradley DJ, Carpenter R, Coen ES;

```

XX WPI: 1997-202235/18.
DR P-PSDB: AAM13945.
XX
XX Antirrhinum majus centroradialis gene and Arabidopsis homologues,
PT Tfl1 - control switching of apical meristem to floral fate, useful
PR in plant hybridisation and in control of growing season
XX
XX Disclosure: Fig 6b; 83pp; English.
XX
CC A genomic clone (AAT60142) codes for the terminal flower 1 (TFL1)
CC protein (AAM13945) of Arabidopsis thaliana. It was obtained from a
CC genomic library using Antirrhinum cen cDNA (see also AAT60139) as
CC probe. A tfl1 cDNA clone (AAT60140) has also been obt. The wild-
CC type role of tfl1 gene is to prevent the apical meristem from
CC switching to a floral fate and to inhibit flowering. The
CC flowering characteristics of transgenic plants, esp. switching
CC of apical meristem to a floral fate and the timing of flowering,
CC can be manipulated by regulating cen or tfl1 gene expression.
CC
XX
SQ Sequence 1430 BP; 446 A; 251 C; 240 G; 493 T; 0 other;

Query Match          9.3%; Score 80; DB 18; Length 1430;
Best Local Similarity 61.5%; Pred. No. 3e-09;
Matches 128; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

OY 590 taaccaagatagaagctcgtgagctctcccaacatcacaactctgtgctttt 649
DB 448 TTACCAAAATGAGAGAGATCTGAGATCCACCATGATCTCAACCTTAGGCTTGAGG 389
OY 650 gaacctgagaagccttagatccaaagcctagtcacacctcttggccataagtaacct 709
DB 388 AACAAGAGAGAGAGAGAGATCTGAGATCCACCATGATCTCAACCTTAGGCTTGAGG 329
OY 710 ttagagtgatgatctatataaacgataagaagcgtctccacaactctgctactataa 769
DB 328 TCATCTTAACTTGTGGAGAGGAATCAAGAACATCTCTCACTCCCATTAATCA 269
OY 770 gaggtctctatattatataagacacct 797
DB 268 ATGGCTCTATCACTACTAGTCCCATATT 241

RESULT 15
AAQ14832/C
ID AAQ14832 standard; cDNA; 822 BP.
XX
AC AAQ14832;
XX
XX 17-DEC-2001 (updated)
DT 25-FEB-1992 (first entry)
XX
XX OV-16 antigen.
DE
XX Onchocerciasis; diagnosis; ss.
KM
XX Onchocerca volvulus.
OS
XX
XX Key Location/Qualifiers
FH CDS 52..510
FT /note= "OV-16 antigenic polypeptide"
FT /tag= a
FT /note= b
FT /tag= b
FT sig_peptide 52..105
FT /tag= c
FT mat_peptide 100..510
FT /tag= d
FT terminator 815..822
FT /tag= e
FT /note= "stem loop structure"
XX

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PN USN7644372-N.
XX
XX 05-NOV-1991.
PD
XX
XX 23-JAN-1991; 91US-0644372.
PF
XX 23-JAN-1991; 91US-0644372.
PR
XX (USSH ) NAT INST OF HEALTH.
XX
XX Lazzeri MSL, Nutman TB, Weiss N;
XX
XX WPI: 1991-361687/49.
DR P-PSDB: AAR15223.
XX
XX Onchocerca volvulus antigen (OV-16) and DNA - useful in early and
PT specific diagnosis of onchocerciasis
PR
XX
XX Disclosure: Fig 4; 48pp; English.
XX
XX The DNA sequence encodes the Onchocerca volvulus antigen (OV-16)
CC which may be used in the diagnosis of onchocerciasis in an animal.
CC Early and specific diagnosis of new or re-infections with O. volvulus
CC in vector reinvasion areas, as well as the detection of light
CC infections in areas where control is being attempted by widespread
CC use of ivermectin, is possible. This allows for monitoring,
CC evaluating and consolidating onchocerciasis control by both the
CC vector control and chemotherapeutic strategies.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis.us.html.)
XX
SQ Sequence 822 BP; 271 A; 142 C; 169 G; 240 T; 0 other;

Query Match          8.4%; Score 71.8; DB 12; Length 822;
Best Local Similarity 51.3%; Pred. No. 2.1e-07;
Matches 217; Conservative 0; Mismatches 202; Indels 4; Gaps 2;

OY 294 ctcccttgacaatgttagaaaacttgcgcacaggaagccgagatgtagatcctcagc 353
DB 637 CTCATGTTTAACTTGAATTTTCGGCATGATTTCCCAAGTATGTTTGTTC 578
OY 354 aaactcgagatgttgaagttctgagc---caacctggtgatacactgttgcctgcc 410
DB 577 AAAATCCATTAACCTTGAATTTTCGGCATGATTTCCCAAGTATGTTTGTTC 518
OY 411 aagctgtgaaacaataataacaacagacagatgaatctctgcagtgagacttgatcttc 470
DB 517 AGGTGTTTATAAACCCAAAGATACATACGATGAAGTCTGTGCTTTTCGTGACCTGA 458
OY 471 gtaacacacatctcatctcgaaggtg-ttccagttgtagaagatataagtcacca 529
DB 457 TCCAAATATCAAGTAACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGA 398
OY 530 accaatgagatattctcggaggtgaggttgcctagagacttgaacatctgatacacca 589
DB 397 ACCAAATGATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGA 338
OY 590 taaccaaagatagaagttcctgaggtctctccaccaactccaactctgctgctgttt 649
DB 337 TAACGAGCCTAATATAAGGCTCCAGGTTCCGATGCCATGATGATTTTGTGCGCTGATCT 278
OY 650 gaacctgagaagccttagatccaaagccttagtcaacctctcttggccataagtaacct 709
DB 277 TTACTGCGTGGCGTAACTGATTCGCCAGATTCACCGTGAGATTATTGTAACAT 218
OY 710 tta 712
DB 217 TGA 215

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Search completed: September 14, 2002, 21:21:27
Job time: 13859 sec

Qy 841 atccactagttcaga 856
 |||||||
 Db 16 ATCCACTAGTTCTAGA 1

RESULT 3
 AB027504/c 864 bp mRNA linear PLN 26-FEB-2000
 LOCUS Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds.
 DEFINITION AB027504
 ACCESSION AB027504.1 GI:4903011
 VERSION FT.
 KEYWORDS Arabidopsis thaliana (strain:Landsberg er) cDNA to mRNA.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
 Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis.
 1 (sites)
 REFERENCE Kobayashi,Y., Kaya,H., Goto,K., Iwabuchi,M. and Araki,T.
 AUTHORS A pair of related genes with antagonistic roles in mediating
 TITLE flowering signals
 JOURNAL Science 286 (5446), 1960-1962 (1999)
 MEDLINE 20050958
 REFERENCE 2 (bases 1 to 864)
 AUTHORS Araki,T. and Kobayashi,Y.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science,
 Kyoto University, Department of Botany, Division of Biological
 Sciences, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 (E-mail:laraqui@gr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136,
 Fax:81-75-753-4141)
 FEATURES
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 /strain="Landsberg er"
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 /chromosome="1"
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 11596-11657, 12371-12411, and 12536-13005 of F5114
 (Accession Number AC001229)"
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 polyA_signal 671..675
 BASE COUNT 284 a 149 c 185 g 246 t
 ORIGIN

Query Match 93.4%; Score 799.6; DB 8; Length 864;
 Best Local Similarity 99.5%; Pred. No. 2.1e-177;
 Matches 802; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 67 tgcacacacacataataagtaaacactcatttccctccctcatttattat 126
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Db 797 TCGCATCACACTATATAAGTAAACACTCTCATTTTCCCTCCCTCTCATTTTATTATTA 738
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 Db 737 CACACTTATATATTGAACACTCTATAGGCATCATCACCCTTCGTTACTCGTATATAAT 678
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 Db 677 GGTTATTAAATTAAATACATATAGATGATCATTAATCTCATAGATGATCATATCATATG 618
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 Db 617 GTTATTAAGGAAGAAGACATCTAAAGCTTCTCTCCGACGCACTCTCCCTGTGACAA 558
 Qy 307 tttagaagaactcgcgcacagggagaagcggagttagatctcagaagaactcgcag 366
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 Db 557 TTGTGAAGAACTGGCGCACGGGAGGCGCAGATGTGAGATCTCAGCAAACTGCGG 498
 Qy 367 ttgaagctcgcgcacacccctgtgtcatcacactgttgcctgcgaagctgcga 426
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 Db 437 ATAAACACGACACAGATGAATTCCTCGACGTGGGACTTGGAATTCGTAAACACAA 378
 Qy 487 ttgcgaaggttgttccagttgtagcagggatatacagtaacacacacatgagat 546
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 Db 377 TTGCCAAGGTTGTTCAGTTGTAGCAGGATATCACTACCAACCAATGAGATATCT 318
 Qy 547 cggagtgagaggtgtctagagacttgcagacatctgcatacacaataacaaataga 606
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 Qy 667 agttccaagcattagcactctctcttgccataagtaacattagagatgatct 726
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 Db 77 ATGACATCTTGATCTTGAACAAC 52

RESULT 4
 AY065378 840 bp mRNA linear PLN 11-DEC-2001
 LOCUS Arabidopsis thaliana putative flowering signals mediating protein
 DEFINITION FT (At1g65480) mRNA, complete cds.
 ACCESSION AY065378
 VERSION AY065378.1 GI:17529185
 KEYWORDS FT1_cDNA.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
 Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis.
 1 (bases 1 to 840)
 REFERENCE Yamada,K., Banb,J., Chang,C.H., Chang,E., Dale,J.M.,
 Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.,
 Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,
 Carinci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamiya,A., Karlin-Neuman,G., Kawai,U., Kim,C., Lam,B.,
 Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
 Sakurai,T., Satou,M., Seki,M., Shimn,P., Southwick,A.,
 Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE	Full Length cDNA of gene Atlg65480 (GI:15218709)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 840)
AUTHORS	Yamada,K., Bann,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Teraiuni,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shimn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE	Direct Submission
JOURNAL	Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The SAIL, Stanford, PGEC (SFP) Consortium members carried out the sequencing and annotation of the RFLV cDNAs: Yamada, K., Banb, J., Chang, C. H., Cheng, E., Dale, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Tordella, M., Wu, H. C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G. G., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Scherck, J. R. and theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologos, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES	SOURCE	LOCATION/Qualifiers
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		/note="This clone is in a modified pBluescript vector (lambda Zap) as a XhoI/SstI insert."
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Query Match	89.28;	Score 763.4;	DB 8;	Length 840;
Best Local Similarity	99.28;	Pred. No. 6.6e-169;		
Matches 767; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0

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Oy	100	atttctctccctctcaattttatcaacaactatataatgaactactataggaatcat	135/146
77b	777	ATTTTCCCTCCCTCATTTTTTTTACACACTTATATTGAACTCTATTAGGCATCAT	71/8

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Db	717	CACCGCTTGCTACTCTCGTATCTCAATAAATGGTTATTTAAATATCTATAGATGCATATAA	658
OY	220	tcctcatcagaaglatcgcatacctaalttggctcaaaagagaagccatctaaagtctctt	279
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OY	280	ccctccgcagccactctccctcttgataaatttctagaataacttggccacgggaagccggaga	339
Db	597	CCTCCGACGCCACTCTCTCCCTGTGAACAATTTGTAAGAAATCGCGCCACGGGAAGCCGGAGA	538
OY	340	cttgatgacatcaagcaaaactcgcgaagtgtctgaagttcttgccgcacccctggctgataact	399
Db	537	TTGTGATGATCTCAGCAAAATCCGCGAGTGTTTGAAGTTCTTGCCGCCACCCCTGGTGCAATACCT	478
OY	400	gtctgcctgcgaagctgtctcgaaacaataataaacacgcagatgaattcctctgcagtggga	459
Db	477	GTTTGTCCCTGCCAAGCTGTGCAAAACAAATATTAACAGCACATGTAATCTCTGCACTGGGA	418
OY	460	cttgatatttcgttaacacacaactcctatctgcgaagcttcttcaggttgtagcagaagta	519
Db	417	CTTGGATTTTGTGTAACACACAACTCTCATTTGCCAAAGGTTGTCCAGTTGTGACAGGGATA	358
OY	520	tcaagtcaccaacccaatgtagatatctctcggaggtgaaggttgcctagaaacttgcgaacact	579
Db	357	TCAGTCACCAACCAATGAGATATTTCTCGGAGGTGAGGTTGCTAGGACTTGGAAACATCT	298
OY	580	ggatccaccataaccaaatatagaagttcctgaagttctctccaccaaatctcaactctt	639
Db	297	GGATCCACCAATTAACCAAAAGTATAGAAAGTTCCTGAGAGTCTTCCCAACCAATCTCAACTCTT	238
OY	640	ggctctgttttcaaaccttggaagaagccttgaatcccaagccatagtaacactcctcttggcca	699
Db	237	GGCTTGTTTGAACCTTGAGAAAGCCTTAGATTCAGCAAGCCATTAGTACCTCTCTTTGGCCA	178
OY	700	taagtaaacctttagatgatatctatctatlaaacggatccaagaacgctctccacaacactt	759
Db	177	TAAGTAACCTTTAGAGTATGATTCATATTTAAACGATCAAGAACGTCCTCCAAACAACCTCG	118
OY	760	cttaactataagaaggtctcttatattatataagacatccttgctcttgaaacaac	812
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[illegible]

Db 348 TCCTCAGTGGGACTTGGATTTCGTACACACAATCTCATTTGCCAAGGTTGTTCCAGT 289
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Db 288 TGTACAGGAGATATCATGTCACCAACCAATGAGATATTTCTCGAGGTGAGGGTTGGTAG 229
Oy 567 acttgaacatctgataccacatacaagaatagaaagttctcgagggtctctccacc 626
Db 228 ACTTGGAACATCTGATCCACATACCAAGTAAGAAGTCTCGAGGCTCTTCACAC 169
Oy 627 aatccactcttgcttgcttgcttgacacgtgaaagacctatagatccaagcttagaac 686
Db 168 AATCTCAACTCTGGCTTGCTTGTGTAACCTGAGAGAGCCCTTAGATCCAGCCATTAGTCAC 109
Oy 687 ctctcttgccataagtaaccttagagtgatgatactataaagcagaacgaacgtc 746
Db 108 CTCTCTTTGGCCATTAAGTAACCTTAGAGTGATGTATTAATAACGAGATCAAGAAGCTC 49
Oy 747 tccaaacactcgtctactataagaagggtctcttataattatagaacat 794
Db 48 TCCAACACACTGCTTACTATTAAGAGGGTCTCTTATATTATAGACAT 1

RESULT 7
F5114/c F5114 109560 bp DNA linear PLN 11-JUN-1997
LOCUS Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1,
DEFINITION complete sequence.
ACCESSION AC001229
VERSION AC001229.1 GI:2182285
KEYWORDS HMG.
SOURCE Thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 109560)
Vysotskaya,V.S., Osborne,B.I., Toriumi,M., Yu,G., Oji,O.,
Shen,Y.K., Buehler,E., Conway,A.B., Conway,A.R., Dewar,K., Feng,J.,
Kim,C., Kurtz,D., Li,Y., Shinn,P., Sun,H., Davis,R.W., Ecker,J.R.,
Federspiel,N.A. and Theologis,A.
The sequence of BAC F5114 from Arabidopsis thaliana chromosome 1
unpublished (1997)
2 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (15-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (17-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (06-JUN-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
5 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (11-JUN-1997)
On Jun 10, 1997 this sequence version replaced gi:1943864.
Location/Qualifiers
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CDS

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gene
CDS

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KLANKGLRRERQOLTRITADIFRLVPAVEITVPEMEFLPEFLKLPNMLPSTFO
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IKTGDDCISIGPCKMLMDGITCGGHHGISLSTLAKSJEBOGVENVYKNAVEFTD
NGRIKSPHRSNPFVPEREALIMVNSYPLIDQNNCPGSSCSOESGKIKINDY
IYSGIMGTSATEIRAIMDCSEKVPCTGIRMOAINLISYGAATSCNTNSGKOLIVT

Query Match 54.4%; Score 466; DB 8; Length 109560;
Best Local Similarity 100.0%; Pred. No. 3.4e-99;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 tatabaataaacacttcatttcacatgtagatbaataataataatcgcacacacataata 85
Db 13000 TATAAATATACACTTCATTTCATGATGATTAATATATATCCATCAGACACTATATA 12941

QY 86 agtaaacacttcatttcctcccccctcattttataaacacactataatgtaact 145
Db 12940 AGTAAACACTCTCATTTTCCCTCCCTCTCATTTTATACACACTTAATATATGAACT 12881

QY 146 actaagaacatcacacgcgttcgtactcgtatcatataaataatggtatataataaac 205
Db 12880 ACTATAGCATCATCACCCTTCCTTACTCGTATCATATAATGTTATTAATTAATATAC 12821

QY 206 tatagatgcataaactcatcaatgaagatgcaataatcattggtataaagaagaagca 265
Db 12820 TATAGATGCATAAATCTCATCAGAGTATGCATAATGTTATGTTAATGAAGAGAACCA 12761

QY 266 tctaagtctcttcctccgcagcgaactctccctcgtacaattgtagaagaactcgcgca 325
Db 12760 TCTAAAGCTCTTCTTCCCTCCGAGCCACTCTCCCTACATAATTTAATAAACTCCGCCCA 12701

QY 326 cgggaagcgcagagatgtagatctcagaactcgcagcgttgaagttctcgcgcacc 385
Db 12700 CGGGAAGCCGACGATTTGTAGATCTCAGCAACTCGCAGTGTTAAGTTCTGGGCCAC 12641

QY 386 ctggtgcatcacactgttgcctgcgaagcgtgcgaacacataataaacagacagatgaa 445
Db 12640 CTGCTGCATCACACTGTTGCTCGTCCGCAAGCTGTCAAAACATATAACACGACGATGAA 12581

QY 446 ttctctgagtgaggaacttggaatttcgtataacacacactcattgcc 491
Db 12580 TTCTCTGAGTGAGGACTTGATTTTGTATACACACAACTCTCATTTGCC 12535

RESULT 8
AF152096/c 2483 bp DNA linear PLN 22-DEC-1999
LOCUS AF152096
DEFINITION Arabidopsis thaliana flowering locus T (FT) gene, complete cds.
ACCESSION AF152096
VERSION AF152096.1 GI:6117977
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosales; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2483)
AUTHORS Kradolsky,I., Shukla,V.K., Ahn,J.H., Dagenais,N.,
Christensen,S.K., Nguyen,J.T., Chory,J., Harrison,M.J. and
Weigel,D.
TITLE Activation tagging of the floral inducer FT
JOURNAL Science 286 (5446), 1962-1965 (1999)
MEDLINE 20050959
REFERENCE 2 (bases 1 to 2483)
AUTHORS Kradolsky,I. and Weigel,D.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
source
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/db_xref="taxon:3702"
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 CDS
 /gene="FT"
 /function="induces flowering"
 /note="similar to hippocampal cholinergic neurostimulating peptide (HCNP) precursor, phosphatidylethanolamine binding protein (PEBP) and Raf kinase inhibitor protein (RKIP); corresponds to Arabidopsis thaliana BAC F5114 sequence presented in Genbank Accession Number AC001229"
 /codon_start=1
 /product="flowering locus T"
 /protein_id="AA03936.1"
 /db_xref="GI:6117978"
 /translation="MSINIRDPILVSRVGDVLDPPRSLIKVYGVREYNGDLR
 PSYONKPRVIEGDDRNRYTLYMVPDPVPSNPRLREYHLHYDIPATTTTGG
 NEVYCNPSPPSGIHRVFLFRQLGRQTVIAPGMQNTREFAIYLDGLPVAAY
 FYNCQRESGGGRRL"
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 BASE COUNT 762 a 391 c 407 g 923 t
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Query Match 54.3%; Score 465; DB 8; Length 2483;
 Best Local Similarity 100.0%; Pred. No. 6.6e-99;
 Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 27 ataataaacattcatctcatgtagatataataatcgcacacacatatataa 86
 Db 2483 ATAAATATAACCTCATTTATGATATATATATATATATATATATATAT 2424
 Oy 87 gtaaaacattcatctcccccctcatctttatataacattatataatga 146
 Db 2423 GTAATAACCTCATTTCTCCCTCTCATTTTATATACACTTATATTTAACTA 2364
 Oy 147 ctataggcatcaacacgcttcgtatcgtatcataaaatggttataataa 206
 Db 2363 CTATPAGCATATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2304
 Oy 207 atagatgcatataatctcatcagagatgcaatataatggttataaagaagac 266
 Db 2303 ATAGATGCAATAATCTCATACAGATATCAATTCATTTGTTATTAAGAAAGCCAT 2244
 Oy 267 cttaagctctctcccgagcacctccctcgtacaattgtagaanaactgcgcac 326
 Db 2243 CTAAGCTTCTTCTCCTCGGACGACCTCTCCCTGACAAATTTGAAAGAACTGGCGGCAC 2184
 Oy 327 gggaagcgcgagatgtatagatcctcaagaactcgcagtgltgaagtlctgcgcaccc 386
 Db 2183 GGGAAAGCGCGAGATTGTGATCTCAGCAAACTCGCGAGTGTGAAGTCTGGCGGCACCC 2124
 Oy 387 tgggtcacatactgttccctgcgcaagctgtcgaanaacttaaacagcaagtgat 446
 Db 2123 TGGTGCATACACTGTTTCCCTGCGCAAGCTGTGGAACAATTAACACAGACAGATGAAT 2064
 Oy 447 tccgtcaatgggaacttgatcttcgtaacacaaatcctcatgccc 491
 Db 2063 TCCTGCACTGGGACTTGGATTTCCTAACACACATCTCATTTGCC 2019

RESULT 9
 AB027506/c AB027506 mRNA linear PLN 26-FEB-2000
 LOCUS Arabidopsis thaliana T5F (TWIN SISTER OF FT) mRNA, complete cds.
 DEFINITION

ACCESSION AB027506
 VERSION AB027506.1 GI:4903015
 KEYWORDS T5F.
 SOURCE Arabidopsis thaliana (strain: Columbia) CDNA to mRNA.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (sites)
 AUTHORS Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.
 TITLE A pair of related genes with antagonistic roles in mediating
 flowering signals
 JOURNAL Science 286 (5446), 1960-1962 (1999)
 MEDLINE 20050958
 REFERENCE 2 (bases 1 to 799)
 AUTHORS Araki, T. and Kobayashi, Y.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science,
 Kyoto University, Department of Botany, Division of Biological
 Sciences, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 (E-mail: taraquiegr.bot.kyoto-u.ac.jp, Tel:81-75-753-4136,
 Fax:81-75-753-4141)
 FEATURES
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 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
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 hippocampal cholinergic neurostimulating peptide (HCNP)
 precursor"
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 /product="T5F"
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 /db_xref="GI:4903016"
 /translation="MSLSRRDPLVGSVGDVLDPPRLVSLIKVYGVREYNGDLR
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 FYNCQRESGGGRRL"
 772..777
 polyA_signal
 BASE COUNT 222 a 152 c 182 g 243 t
 ORIGIN
 Query Match 45.5%; Score 389.8; DB 8; Length 799;
 Best Local Similarity 76.6%; Pred. No. 3e-81;
 Matches 505; Conservative 0; Mismatches 147; Indels 7; Gaps 2;
 Oy 157 catcacgcttgctactcgtatcataaataatggttataataaata----ctatagatg 213
 Db 676 CATCATTTTTTTTACTCGTATCTTAATTCCTTATATACATGACATGATCTTAATA 617
 Oy 214 cataaatctcatcagagatgcaatataatcattggtataaagaagaag----ccatcta 269
 Db 616 CTTCAATTAAAGGAATATTATACGATTAGATTATTAAGTTAAAGTAGTACCATCTTA 557
 Oy 270 aagctctctcccgagcacctccctcgtacaattgtagaanaactgcgcacaggg 329
 Db 556 CGTTCTTCTCCCGACAGCATTTCTCCCTGCGCAGTTGAAGTGAAGAGCAGCAGCAGG 497
 Oy 330 aagcgcgagatgtatagatcctcaagaactcgcagtgltgaagtlctgcgcacccctgg 389
 Db 496 AAGACCAAGATTGTGATCTCAGCAAACTCAGATGTGTAACCTGTTGGCCGACCCCGG 437
 Oy 390 tgcataacgttcccgcaagctgtcgaanaacttaaacagcaagatgaatcc 449

Db 436 TGCATAAACCGTTTGTCTCCGAGTTGCCGAAACATACCAACAAATACGATGATTC 377
QY 450 tgcagtgaggacttggaatttccttaacacacacatctatccaaaggttgctcaagttgt 509
Db 376 CGAGGGGGGACGTGACTCTCGTAGCACACCACTCAATGCCAAAGGCAATTTCCAGTGT 317
QY 510 agcagagatactcagtcaccaacatgagatattcccgaggtggaaggttgctaggact 569
Db 316 GGCAGGATATTCAGATCCACCAACAGTGAGATATTCGTTGGAGAGGTTGCTGGACT 257
QY 570 tggacaactcgtgatccacataaccaagaatagaaagttcctgaggtctctccacaat 629
Db 256 CGGCACATCTGATCCACCAATCAAGGTGTAGAAATTTCTGAAATTCGCTCCCAAT 197
QY 630 ctcaactcgtgctgtgtttgaacctgaagaaggtcttaagtcgaagcattatgcactc 689
Db 196 CTCACATATGTTGTTGTTCAGAACTTGAGAGGCTTAGATCCAAAGCATTAGAACCTC 137
QY 690 tcttggcacaatgaactccttagagtgatgatctatctaaacgagatcaagacgtctcc 749
Db 136 TCTATGGCCATTAAGTACCTTAAGAGAGACCAACCTCGTGAAAGATCAAGAACATCTCC 77
QY 750 acaaacctcgtactataaagaaggtctcttataattatagaactcttgatctgaac 808
Db 76 AACAACTGCTCCGACCAAGAGGATCTCTAGCACTTAAGACATATTATCTTGATC 18

RESULT 10
AF152907/c 528 bp mRNA linear PLN 22-DEC-1999
LOCUS Arabidopsis thaliana twin sister of FT (TSP) mRNA, complete cds.
DEFINITION AF152907
ACCESSION AF152907
VERSION AF152907.1 GI:6117979
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 528)
Kardailsky,I., Shukla,V.K., Ahn,J.H., Dagenais,N.,
Christensen,S.K., Nguyen,J.T., Chory,D., Harrison,M.J. and
Weigel,D.
Activation tagging of the floral inducer FT
Science 286 (5446), 1962-1965 (1999)
20050959
TITLE 2 (bases 1 to 528)
JOURNAL Haaksma,S., Shukla,V.K., Ahn,J.H. and Weigel,D.
Direct Submission
Submitted (19-MAY-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES
source
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Location/Qualifiers
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="IV"
/map="between g3883 and g13838"
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/gene="TSP"
1..528
/note="flowering locus T (FT) homolog; similar to
hippocampal cholinergic neurostimulating peptide (HCNP)
precursor, phosphatidylethanolamine binding protein (PEBP)
and Raf kinase inhibitor protein"
/codon_start=1
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/protein_id="AF03937.1"
/db_xref="GI:6117980"
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PSQVLNKPIVEIGDDFRNFYTLVMWDPVSPSPNPQREYLLHMLVTDIPATGNMAG

BASE COUNT 123 a 116 c 142 g 147 t
ORIGIN
NEVCYESPPSPGIRHIVLFLRQLGROTVVAPGRQOFNTRFEAIYNLGPVNAS
YFNCORENGCGGRRT"
Query Match 44.1%; Score 377.6; DB 8; Length 528;
Best Local Similarity 82.2%; Pred. No. 2.2e-78;
Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 267 ctaaagctcttcctccgcagacacatccctccctgcacaattgataaactcgcgcac 326
Db 528 CTACGTTCTTCTTCCCCACAGCCATTCCTCCTCGAGTTGAAGAGGACGAC 469
QY 327 gggagagcagagatttgatgactcagaactcgcaggttgatgaagttcggccacc 386
Db 468 AGGAGAGCAAGATGTAGATCTCAGCAAACTCAGAGTGTGAAGTGTGGCCACC 409
QY 387 tggatcacactgttgcctcccaagctgtcgaacaataaacaagacagatgaat 446
Db 408 CGGTGCAATAAACGTTTGTCTCGAGTTGCCGGAACAATACCAATACGATGAAT 349
QY 447 tctcgcagtgagacttggaatttcgtaacacacatctcatcgaaggttgctcagt 506
Db 348 TCCGAGGGGGGACGTGACTCTGTAGCACACCACTCAATGGCAAGGATTTCCAGT 289
QY 507 tgtagcagggatcagtcacacacacaaatgagatattctcggaggtggaaggtgtcagg 566
Db 288 GGTGGCAGATATATCAGTCACCAACCACTGGAGATATTTCTGTTGGTAGGGTTGCTGG 229
QY 567 acttgaacactcgtgatccacacataaacaagataagaagttcctgaggtctccacc 626
Db 228 ACTCGGCACATCTGGATTCACCAACCAAGTGATTAATTTCTGGAAGTGTCTCTCC 169
QY 627 aatccaactctggtctgttctgaacctgaagaagccttagatccaaagcattagtcac 686
Db 168 AATCTCCACTATTTGTTGTTCACAACTTGAAGGCGCTTAGATCCAAAGCATTAGTAAC 109
QY 687 ctctccttgccataaagtaaccttagagtagtatgactatctaaagatcaagaagctc 746
Db 108 CTCTCTATGGCCATTAAGTGAAGTGAAGAGACCAACTCGTGAAGGATCAAGAACATC 49
QY 747 tccaacactctgtactataaagaaggtctcttataattatagaacat 794
Db 48 TCCAACAAGACTGCCGACCAAGAGGATCTCTAGCACTTAAGACAT 1

RESULT 11
E38986/c 528 bp DNA linear PAT 31-JAN-2002
LOCUS E38986
DEFINITION Method for shortening plant generation and plant.
ACCESSION E38986
VERSION E38986.1 GI:18625005
KEYWORDS JP 2000139250-A/2.
SOURCE JP 2000139250-A/2.
ORGANISM Arabidopsis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae.
1 (bases 1 to 528)
Araki,T., Kobayashi,K., Ogawa,K. and Shirai,M.
Method for shortening plant generation and plant
Patent: JP 2000139250-A 2 23-MAY-2000;
TORAY IND INC
OS Arabidopsis
PN JP 2000139250-A/2
PD 23-MAY-2000
PR 11-MAY-1998 JP 1998320219
PI TAKASHI ARAKI, KYOJI KOBAYASHI, KENICHI OGAWA, MAKOTO SHIRAI PC
A01H1/00,A01H5/00,C12N5/10,C12N15/09//C12N5/10,C12R1:91), PC
(C12N15/09,C12R1:91),C12N5/00,C12N15/00,C12N5/00,C12R1:91), PC
(C12N15/00,C12R1:91)

CC Key Location/Qualifiers
FH source 1..528
FT /organism="Arabidopsis".
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source 1..528
/organism="Arabidopsis"
/db_xref="taxon:3701"

BASE COUNT 122 a 117 c 142 g 147 t

ORIGIN

Query Match 43.7%; Score 374.4; DB 6; Length 528;
Best Local Similarity 81.8%; Pred. No. 1.3e-77;
Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY 267 ctaagctctctccgcagccactccctccctgcacatgtagaagaactgcgagccac 326
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DB 528 CTAGCTTTCTTCTCCACAGCCATTCTCCCTTGCGAGTTGAAGGACAGCCAC 469
OY 327 gggaagccgagatgtatgatctcagcaaacctcgagtgltgaaagtctgcgacacc 386
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DB 468 AGGAAGACCAAGATGTAGATCTCAGCAACCTCAGAGAGTTGAACGTGTGGCCGACCC 409
OY 387 tgytgcataacatgttctccgcgcaagctgtcgcgaacaataaacacagacagatgaat 446
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DB 408 CGGTGCATTAACCGTTGTCTTCCAGTGTGCGGAACAATACCAACACATACGATGAAT 349
OY 447 tccctcagtggaacttgatcttcgtaacacaaatccatcattgcgaagtgctccagt 506
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DB 348 TCCCGAGGGGAGCTGAGACTCTCTAGCACACACCTCATTTGCCAAGGCAATTTCCAGT 289
OY 507 tctagcagagatcatcagtcacaaacaaatggagatatctcggaggtagaggttgcag 566
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DB 288 GGTGCGACAGTATATCAGTACCAACCACTGAGATATTCTGTTGTGAGGGTTCTTGG 229
OY 567 acttggaacactgagatccacataccaagaatagaagtctcgaagctctccacc 626
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DB 228 ACTGCGCATTCAGATCACCATTACCAAGGTGTAAGAAATTTCTGAAGTCTCTCTCC 169
OY 627 aatctcaactcttgctgttcttggaaccttggaagagccttagatccaaagccatgac 686
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DB 168 AATCTCCCATATGTGGTTGTTCAGAACTTGAAGAGCCTTATGATCCAGCCATTAGTAA 109
OY 667 ctctcttgagcacaatgaaccttaagtgatgtatctataaagcgaatcaagaagctc 746
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DB 108 CTCTCTAAGGCGATTAAGACCTTAAGAGAGCAACCTCGTGAAGGATCAAGAACATC 49
OY 747 tccaaacactctgctactataaagaggtctctatatattatagaacat 794
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DB 48 TCACACACACTGCCGACACGAGAGATCTCTACGACTTAAGACAT 1

RESULT 12
AB027456/c 745 bp mRNA linear PLN 26-FEB-2000
LOCUS Citrus unshiu ClFT mRNA, complete cds.
DEFINITION AB027456
ACCESSION AB027456
VERSION AB027456.1 GI:4903138
KEYWORDS ClFT.
SOURCE Citrus unshiu (strain:Miyagawa-wase satsuma mandarin) developing stage juice sac and pulp segment cDNA to mRNA.
ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE
AUTHORS Kobayashi,Y., Kaya,H., Goto,K., Iwabuchi,M. and Arai,T.
TITLE A pair of related genes with antagonistic roles in mediating flowering signals
JOURNAL Science 286 (5446), 1960-1962 (1999)
MEDLINE 20050958
REFERENCE 2 (bases 1 to 745)

AUTHORS Omura,M., Kobayashi,Y. and Arai,T.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1999) Mitsuo Omura, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu, Shimizu, Shizuoka 424-0292, Japan (E-mail:om9330@okt.affrc.go.jp, Tel:81-543-69-7108, Fax:81-543-69-2115)
FEATURES
source 1..745
/organism="Citrus unshiu"
/strain="Miyagawa-wase satsuma mandarin"
/db_xref="taxon:55188"
/dev_stage="developing stage juice sac and pulp segment"
/note="Partial sequence (pcwfr172.131) is deposited in Accession Number C24153"
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/note="Extensive homology to FT (FLOWERING LOCUS T, AB027504) and TSF (TWIN SISTER OF FT, AB027506) genes of Arabidopsis thaliana; similar to mammalian phosphatidylethanolamine binding protein (PEBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor"
/codon_start=1
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BASE COUNT 195 a 150 c 180 g 220 t

ORIGIN

Query Match 33.8%; Score 289.6; DB 8; Length 745;
Best Local Similarity 72.3%; Pred. No. 9.8e-58;
Matches 376; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

OY 277 ctctccgcagccactctccctctgacaattgtgaanaactgcgcgcaggaagcg 336
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DB 613 CTTCGCGGAGATCCGCTCCTCCCTGCGAGTTGAAGTAGACAGCGGCCACCGAGAGTCC 554
OY 337 agatgtatcatctcagcaaacctcgagtgltgaaagctctgcgcacacctggtgcatac 396
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DB 553 AGATTGTAAAGCTCAGCAAAATCCCTCGTGAAGTCTGACGCGCACCTGTGCATTA 494
OY 397 actgttgcctgcgaagctgtcgcgaacaataaacaagcagcagatgaattccctgcagt 456
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DB 483 ACAGTCTGCTCCCAAGTTCGCGGAACAACAAAGACAAACCTGTGAATCCCATCTT 434
OY 457 ggaacttgattctgtaacacacaatctcaatgcgaagtgltccagttagcagg 516
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DB 433 GGCCCTAAGGCTTTCTATGATTCACATCTCTGGCCAAAGCTGGCCCTGTGTTCTGGA 374
OY 517 atatagcacacaacaaatgagatatctcggaggtgaaggttgcgtagagcattggaaca 576
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DB 373 ATATCAGTCACCAACCATGCAAAATCTCCCTAAAGCTGGGCTCACTTGGCTTGCA 314
OY 577 tctgataccacataaacaagaatagaagttcctcgaagctctctccacaactcacaact 636
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DB 313 TCAGATATCAACCATTAACCAAGTATATAATGTCTTAAGATCATACCAATTTACACC 254
OY 637 cttagctgttcttgaaacctgaagagccttagatccaaagcattagtaacctctcttgg 696
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DB 253 CTAGGCTGTGTCAGAACTTGAAGAGTTGAGTCACGCGCATTAATTAATCTCTGTTT 194
OY 697 ccaataagaaccttagagtgatgtatctataaagcgaatcaagaagctctccacaact 756
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DB 193 GAATAGTAAATCCATTCATTTGAATGTTCTTGTAAATTTGCAAGAACATCAACCAACG 134
OY 757 ctgctactataaagaggtctctatatattatagaacatc 796
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Db	133	C6GCCAACAATPAGAGATCTCTCCCTGCTACACATAT	94
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RESULT	13		
LOCUS	ABO52943	847 bp	mRNA linear PLN 21-JUN-2001
DEFINITION	Oryza sativa Hd3a mRNA, complete cds, cultivar:Kasalath.		
ACCESSION	ABO52943		
VERSION	ABO52943..1	GI:14517621	
KEYWORDS			
SOURCE			
ORGANISM	Oryza sativa (cultivar:Kasalath) cDNA to mRNA.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriharoidae; Oryzaceae; Oryza.		
AUTHORS	Kojima,S., Monna,L., Fuse,T., Sasaki,T. and Yano,M.		
TITLE	Hd3a, a quantitative trait locus, involves in the promotion of flowering in rice		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 847)		
AUTHORS	Yano,M. and Kojima,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-DEC-2000) Masahiro Yano, National Institute of Agrobiological Resources, Department of Molecular Genetics; 2-1-2 Kamohara, Tsukuba, Ibaraki 305-8607, Japan (E-mail:myanoeabr.aifrc.go.jp, Tel:81-298-38-7443, Fax:81-298-38-7468)		
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ACCESSION	AB052944		
VERSION	AB052944.1	GI:14517623	
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ORGANISM	Oryza sativa		
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; Ehrhartoideae: Oryzaceae; Oryza.		
AUTHORS	Kojima,S., Monna,L., Fuse,T., Sasaki,T. and Yano,M.		
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REFERENCE	2 (bases 1 to 847)		
AUTHORS	Yano,M. and Kojima,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-DEC-2000) Masahiro Yano, National Institute of Agricultural Resources, Department of Molecular Genetics; 2-1-2 Kamonodai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:myano@agr.affrc.go.jp, Tel:81-298-38-7443, Fax:81-298-38-7468)		
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 DEFINITION Oryza sativa RFT1 mRNA for FT-like protein, complete cds.
 ACCESSION AB062676
 VERSION AB062676.1 GI:17221651

SOURCE
 ORGANISM Oryza sativa (cultivar: Nipponbare) cDNA to mRNA.
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (sites)
 Kojima, S., Lisa, M., Takahashi, Y., Sasaki, T. and Yano, M.
 The photoperiod sensitivity gene Hd3a promotes flowering in rice
 downstream of Hd1
 unpublished
 2 (bases 1 to 866)
 Yano, M. and Kojima, S.
 Direct Submission
 Submitted (01-JUN-2001) Masahiro Yano, National Institute of
 Agricultural Sciences, Department of Molecular Genetics; 2-1-2
 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail: myano@nias.affrc.go.jp, Tel: 81-298-38-7443,
 Fax: 81-298-38-7468)

FEATURES
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